

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:52 ; Search time 53.5 Seconds
(without alignments)
901.621 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863
Sequence: 1 MASLGLTALAAATLAPFGA.....VELVAIVNPSSALSPDSIKM 362

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq_101002:*
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	16 AAM00635	ILTV glycoprotein
2	1863	100.0	362	17 AAM06787	ILTV glycoprotein
3	156	8.4	384	15 AAR47236	Wild-type feline H
4	152	8.2	355	18 AAM13105	Marek's disease vi
5	152	8.2	355	18 AAM11475	Marek's disease vi
6	148	7.9	364	18 AAM22999	Canine herpesvirus
7	148	7.9	364	19 AAM72659	Canine herpes viru
8	148	7.7	364	22 AAB51316	Pseudorabies virus
9	143.5	7.7	350	8 AAP0645	Glycoprotein 63 (g
10	143.5	7.7	350	15 AAR63143	

11	143.5	7.7	350	22 AAE05396	Pseudorabies virus
12	143	7.7	317	16 AAR80637	Bovine herpes viru
13	142.5	7.6	350	22 AAU04970	Pseudorabies virus
14	141.5	7.6	350	22 AAB82502	Pseudorabies virus
15	140.5	7.5	380	15 AAR48063	Sequence of polype
16	139	7.5	371	22 AAB78825	Pseudorabies virus
17	138	7.4	370	21 AA32474	DNA encoding feli
18	125	6.7	356	17 AAM03136	Herpesvirus of tur
19	125	6.7	356	17 AAM03323	Herpesvirus of tur
20	123.5	6.6	436	13 AAR32160	Meiok Disease Viru
21	114	6.1	456	14 AAR33181	Human secreted pro
22	112	6.0	387	20 AAY06812	Human secreted pro
23	112	6.0	387	21 AAY63312	Human secreted pro
24	109.5	5.9	454	14 AAR33181	LD14 mutant M8.
25	108.5	5.8	319	22 AAB65348	Drosophila melanog
26	108	5.8	319	22 AAB65348	ND-40 domain contg
27	107	5.7	372	16 AAR85878	HSV-2 strain SB5 C
28	107	5.7	372	19 AAW72164	HSV-2 strain SB5 C
29	107	5.7	433	19 AAW72012	Human polypeptide
30	105.5	5.7	378	22 AAM39027	Drosophila melanog
31	103	5.5	982	22 AAB58158	Human secreted pro
32	102.5	5.5	379	20 AAY25768	Human ORF280 prot
33	102.5	5.5	4498	22 AAB58595	Human ORF280 prot
34	102	5.5	503	12 AAR14768	Metastasis-specifi
35	98	5.3	234	23 AAB33907	Drosophila melanog
36	97.5	5.2	1714	22 AAB60186	Human novel polype
37	96	5.2	1296	23 AAB66702	Human novel polype
38	96	5.2	1296	23 AAB66702	Drosophila melanog
39	95	5.1	745	22 AAB71016	Human novel polype
40	94.5	5.1	307	19 AAB38334	Kat kidney injury
41	94	5.1	886	22 AAB64308	Drosophila melanog
42	93.5	5.0	907	6 AAP50073	Epsstein-Barr virus
43	93.5	5.0	907	16 AAR80144	Epsstein-Barr virus
44	93.5	5.0	907	21 AAY68009	Epsstein-Barr virus
45	93	5.0	320	22 AAG91867	C glutathion prote

ALIGNMENTS

RESULT 1	
AAW0635	standard; Protein: 362 AA.
ID	AAW0635
XX	AAW0635;
XX	19-NOV-1996 (first entry)
XX	ILTV glycoprotein gl.
DE	Infectious laryngotracheitis virus; ILTV; herpesvirus;
XX	attenuation; vector: vaccine; chicken; poultry; immunisation;
KW	glycoprotein gl.
XX	
XX	Infectious laryngotracheitis virus.
OS	
XX	MO9508622-AL.
XX	30-MAR-1995.
XX	16-SEP-1994; 94MO-US10628.
XX	24-SEP-1993; 93US-0126597.
XX	
XX	(SYTR) SYNTRO CORP.
XX	Cochran MD, Wild MA:
XX	WPI: 1995-139591/18.
XX	N-PSDB: AAT33504.
XX	Recombinant attenuated infectious laryngotracheitis virus - for use
PT	in vaccines to protect poultry from infection from the virus, also

PT methods of distinguishing between vaccinated and naturally infected
birds

Example 1: Page 102-103; 177pp; English.

CC The gi gene, spanning nucleotides 9874-10962 of the unique short
CC region (AAT33504) of infectious laryngotracheitis virus (ILT),
CC codes for a glycoprotein (AAM06787) of approx. 39,7535 mol.wt.
CC The gi glycoprotein is homologous to Varicella-zoster gi.
CC Deletion of the gi gene results in an attenuated ILTV that
CC is useful as a vaccine against ILT disease in chickens.
CC Recombinant virus deleted for gi was safe in animal trials.
CC Deletion of the gi gene serves as a negative marker to
CC distinguish vaccines from infected animals. A gene coding
CC for a foreign antigen may be inserted into the gi gene to
CC produce a recombinant multivalent vaccine.

SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 16; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIQLDFMPGQ 60
DB 1 MASLGLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIQLDFMPGQ 60
QY 61 RPHKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 61 RPHKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 121 PPHPEFLITRNPRPNDSGMFYIVRLDTPKEPIDVAIQLSVQFANTATRGLYSKASC 180
DB 121 PPHPEFLITRNPRPNDSGMFYIVRLDTPKEPIDVAIQLSVQFANTATRGLYSKASC 180
QY 181 RTFGLPTVLEAVLRTSESRMNOAVVATEATTSAEATTPPVATSAEAEHFTTP 240
DB 181 RTFGLPTVLEAVLRTSESRMNOAVVATEATTSAEATTPPVATSAEAEHFTTP 240
QY 241 WLENGVDHYEPTPANENSVTVRLGTMSPTLIGVTVAAVSATIGLVISITVRMCTP 300
DB 241 WLENGVDHYEPTPANENSVTVRLGTMSPTLIGVTVAAVSATIGLVISITVRMCTP 300
QY 301 HKRLDVSODDERSGTRESKRFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HKRLDVSODDERSGTRESKRFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 2

AAM06787
ID AAM06787 standard; Protein; 362 AA.

AC AAM06787;

DT 02-JUN-1997 (first entry)

DE ILTV glycoprotein gi.

KM ILTV; vaccine; vector; attenuation; poultry;

KM avian infectious bronchitis virus; Newcastle disease virus;

KM infectious bursal disease virus of chickens;

OS Infectious laryngotracheitis virus USDA strain 8302.

XX Key Location/Qualifiers

FT Peptide 1..22

FT Protein 23..362

FT Region /label= Mat_protein
FT 272..292

XX W09629396-A1 /label= Transmembrane_helix

XX 26-SEP-1996.

XX 21-MAR-1996; 96WO-US03916.

XX 06-JUN-1995; 95US-0468190.

XX 23-MAR-1995; 95US-0410121.

XX (SYTR) SYNTRO CORP.

XX Cochran MD, Wild MA;

XX MPI: 1996-443172/44.

XX N-PSDB; AAT44384;

XX N-PSDB; AAT44385.

PT Recombinant infectious laryngotracheitis virus with deletion in the

PT glycoprotein G, gi or us2 gene, etc. - useful for vaccines against

PT infectious laryngotracheitis in poultry

PS Example 11: Page 110-111; 216pp; English.

CC Glycoprotein gi (AAM06787) is encoded by ORF8 of the unique short
CC region (AAT44384) of infectious laryngotracheitis virus (ILT). It
CC shows homology to the Varicella zoster virus gi glycoprotein.
CC Recombinant ILTV gi protein produced in a swinepox virus reacts to
CC convalescent sera from ILTV-infected chickens. Deletion of the gi
CC gene results in an attenuated ILTV that is useful as a vaccine and
CC as a negative marker to distinguish vaccinated from infected
CC animals. Insertion of a foreign gene into the gi gene allows
CC prodn. of multivalent vaccines.

SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 17; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIQLDFMPGQ 60
DB 1 MASLGLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIQLDFMPGQ 60
QY 61 RPHKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 61 RPHKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 121 PPHPEFLITRNPRPNDSGMFYIVRLDTPKEPIDVAIQLSVQFANTATRGLYSKASC 180
DB 121 PPHPEFLITRNPRPNDSGMFYIVRLDTPKEPIDVAIQLSVQFANTATRGLYSKASC 180
QY 181 RTFGLPTVLEAVLRTSESRMNOAVVATEATTSAEATTPPVATSAEAEHFTTP 240
DB 181 RTFGLPTVLEAVLRTSESRMNOAVVATEATTSAEATTPPVATSAEAEHFTTP 240
QY 241 WLENGVDHYEPTPANENSVTVRLGTMSPTLIGVTVAAVSATIGLVISITVRMCTP 300
DB 241 WLENGVDHYEPTPANENSVTVRLGTMSPTLIGVTVAAVSATIGLVISITVRMCTP 300
QY 301 HKRLDVSODDERSGTRESKRFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HKRLDVSODDERSGTRESKRFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 3

AA047236
ID AAR47236 standard; Protein: 384 AA.
XX
AC AAR47236;
XX
DT 06-SEP-1994 (first entry)
XX
DE Wild-type Feline Herpes Virus ORF-1-encoded protein.
XX
DE Feline herpes virus; FHV; genome; mutant; vaccine; ORF-1;
XX
KM Feline viral rhinotracheitis; herpesviridae family;
XX
KW herpes virus A subfamily.
XX
OS Feline Herpes Virus.
XX
PN MO9403621-A.
XX
PD 17-FEB-1994.
XX
PD 23-JUL-1993; 93MO-EP01971.
XX
PR 30-JUL-1992; 92EP-0202365.
XX
PA (ALKU) AKZO NV.
XX
PI Sondermeijer PJA, Willemse MJ;
XX
DR WPI: 1994-065709/08.
XX
DR N-PSDB: AA056188.
XX
PT Feline herpes virus mutant comprising a heterologous gene
XX
PT inserted in the virus genome - for vaccination against feline
XX
PT herpes virus and other feline pathogens.
XX
PS Claim 2; Page 37-38; 55pp; English.
XX
CC Mutant versions of the wild-type feline herpes virus genome (AA056188)
XX
CC are claimed. Esp. the FHV mutant is one which fails to produce one
XX
CC or more antigenic or functional polypeptides. The mutant may contain
XX
CC a heterologous nucleic acid sequence inserted within one of the 6
XX
CC open reading frames. The attenuated FHV mutants can be used to prepare
XX
CC vaccines against feline viral rhinotracheitis and, where the
XX
CC heterologous insert encodes an antigen of a feline pathogen,
XX
CC against other infectious diseases of felidae.
XX
SQ Sequence 384 AA:
XX
Query Match 8.4%; Score 156; DB 15; Length 384;
Best Local Similarity 23.3%; Pred. No. 1.6e-06;
Matches 75; Conservative 48; Mismatches 141; Indels 58; Gaps 12;
OY 5 LGTLLAATLAPFGAMGIVTGNHVSARIDDDHIVAPRPE-ATIQLOLFMPGQ-RP 62
DB 1 MSSIAFTYILMAIGTVIGIVRGDHSLNVDSSGFIYPTLENTTIGHLIFLDQPLP 60
OY 63 HKRYSGTVAVAFRSDITNOCYQELSEERFENCTHSSSVFPGC--KTEYTFASNRLLG 120
DB 61 VNNINGTLEI-ITHNHSSCKYIVQVIEYSSCFRRANRNFSCIAKTSMDIQOLISINTS 119
OY 121 PPHFKITRNPRPNDGMEYVIVRLDDTKEPIDVFAIOLSVQFANTATRGLYSKASC 180
DB 120 VETGMILTTTSPRMDGGIYALRVRFNNNRK-ADVAGLSVEYSP---DTRGHRHAD- 173
OY 181 RTGGLPVOLEAVLYRTESMRNQAVYATVATTSSEATPTPVATASAELEAEHFTFP 240
DB 174 -----ENNGEILITPS--SMETVYKVTPIYDHMVTQ---TSNMSME---P 216
OY 241 WLENGVDHEPTTPANDNSNVTVRL-----GTMSPTLLGVVAVAVVSAT- 283
DB 217 SNTSISCHTFQNDPNEGEGLYTHLNLINAGNITYDDVMADGTTIAPRLIDMGLNLSYSSSP 276
OY 284 -----IGLVYIYSI 292
: | | | | |

DB 277 KNETTQKWTDPDRKGVFIYISI 298
RESULT 4
ID AAM13105
XX
AC AAM13105 standard; Protein: 355 AA.
XX
DT 12-MAY-1997 (first entry)
XX
DE Marek's disease virus type 1 glycoprotein I.
XX
DE GA strain; glycoprotein; gpI; gpE; recombinant virus;
XX
KM Newcastle disease virus; herpes virus; vaccine.
XX
OS Marek's disease virus type 1.
XX
PN JP09009978-A.
XX
PD 14-JAN-1997.
XX
PD 26-APR-1996; 96JP-0131084.
XX
PR 28-APR-1995; 95JP-0129523.
XX
PA (JAPC) JAPANESE GEON CO LTD.
XX
DR WPI: 1997-126432/12.
XX
DR N-PSDB: AAT61883.
XX
PT Recombinant virus contg. herpes virus glyco:protein gpE - and
XX
PT effective Newcastle disease vaccine contg. it
XX
PS Claim 5; Pages 14-15; 20pp; Japanese.
XX
CC The present sequence encodes the Marek's disease virus (MDV) type 1
XX
CC (GA strain) glycoprotein (gpI). A recombinant virus containing the
XX
CC gene encoding MDV gpE, and optionally also gpI, in a genomic region
XX
CC unessential for its growth, can be used as the effective component
XX
CC in a Newcastle disease virus vaccine.
XX
SQ Sequence 355 AA:
XX
Query Match 8.2%; Score 152; DB 18; Length 355;
Best Local Similarity 22.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;
OY 19 GAMGIYITGNHVSARIDDDHIVAPRPE-ATIQLOLFMPGQRPKRGIVAVAFRSD 77
DB 15 GIMSIYITGTSVLTSTDSALVAFCGIDKKVNVNROGLFLDDQRTSSYGTTEL-LKWD 73
OY 78 ITNOCYQELSEERFENCTHSSSVFVCGKTEYTESASNRLLGPPHFK--LIRNRP 134
DB 74 EEYKCVSLHATSYMDCPAIDATVAFRCRDVAVVYAOPIHRYV--OPFEKGTLLRIYEPV 131
OY 135 NDGMPYVIVRLDDTKEPIDVFAIOLSVQFANTATRGLYSKASCRTFGLPTVOLEAVL 194
DB 132 SDGSGYIVVALAG--RNMSDIFRMAVIRIS-----SKSWACHNSASSFOAKCI 179
OY 195 RTEE--SWRNQAVYATVATTSSEATPTPVATASAELEAEHFTPWLNGVDHVEPT 252
DB 180 RYVDRAFERNYLIGHVGLDSDSELAIAINIPQIS--TOINITTPFDNGSTIYSP 238
OY 253 P---ANENSVIVRGLT--MSPTLLGVVAVV--SATIGLVIV--ISITRNMCPPHKK 303
DB 239 VENLFNNSHVNDAMNSTMNTVLAKTPLRPLIFSMIVLCIALAIYIVCEGRCBPHRR 298
OY 304 LDTVSODDERSGOTRRSRKRGFPWACEIKKGDQSELYE 344
DB 299 I---YIGEPFSD-----APLTSANVESFOYIYNKE 328
: | | | | |

RESULT 5
AAW11475
ID AAW11475 standard; Protein: 355 AA.
XX
AC AAW11475;
XX
DT 30-APR-1997 (first entry)
XX
DE Marek's disease virus glycoprotein gI.
XX
MDV; UL32; membrane glycoprotein 82; glycoprotein gI; antigen;
KM vaccine; vector; fowlpox virus.
XX
OS Marek's disease gammaherpesvirus type 1 strain GA.
XX
PN WO9703187-A2.
XX
PD 30-JAN-1997.
XX
PF 05-JUL-1996; 96WO-US11360.
XX
07-JUL-1995; 95US-0499474.
PA (JAPG) NIPPON ZEON KK.
PA (USDA) US SEC OF AGRIC.
XX
PI Lee LF, Nazerian K, Witter RL, Wu P, Yanagida N;
PI Yoshida S;
XX
DR WPI; 1997-119044/11.
XX
PT New DNA encoding glycoprotein 82 of Marek disease virus - useful in
PT vaccines to protect poultry
XX
PS Disclosure; Page 72-73; 101pp; English.
XX
CC Genes encoding Marek's disease virus glycoprotein gI (AAW11475)
CC and/or glycoprotein gE (AAW11474) can be incorporated into
CC recombinant viral vectors that also carry the UL32 gene (see also
CC AAT51358) encoding glycoprotein 82 (AAW11473). The gI and gE genes
CC were cloned from MDV genomic DNA by PCR (see also AAT51366-69 and
CC AAT51366-67). A transfer vector was constructed that was used to
CC produce a recombinant fowlpox virus useful as a vaccine to
CC protect poultry against MDV infection.
XX
SQ Sequence 355 AA:
Query Match 8.2%; Score 152; DB 18; Length 355;
Best Local Similarity 22.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;
19 GAWGIVITGNHVSARIDDDHIVYVAPRPE-ATIQQLFFMPCQRPKPYSGTVRVAFRSD 77
15 GIMSIYVTGVSVALSTDSALVAFGLDKMNVNRQLLFLGDTTRSSVTGTETI-LKMD 73
78 ITNOCQOEISEEFENCNTHRSSVFCVETETESASNRLLGPPHPEK--LTINPRP 134
74 EEKCKSVLHATSYMDCPAIDATVEFRCDAVVAQPHDRV--QPPPEKGTLLRIIVEPV 131
135 NDSGMFVYVRLDDTKEPIDVFAIOLSVQFANTATRGVYASASRTGGLPYOLEAVL 194
132 SDIGSYITVALAG-RNMSDIFRMAVILNS-----SKSMACNHSASSFOAHKCI 179
195 RTEE--SMRNMOAYVATEATTSAEATPTPVATASASELEAHFTFPMLENGVDHYEPT 252
180 RYVDRAAFENYLIGHGNLDSDELHAIYINITPOS--TDINIITTPYDNGTITSPT 238
253 P--ANENSNVVRLGT-MSPTLIGVAAV--SATIGLVV--ISIVTRNMTCPHKK 303
239 VNFLFNNSHVDAMNSTMGMNTVLKYLTPRLIYFTMIYICIAIALIYVCERCSPHRR 298
304 LDTVSODDEERSQTRRESKRFQPMVACEINKGADDSOLVE 344

DB 299 I-----YIGEPKRSDE-----APLITSAVNESFOYDYNKE 328
RESULT 6
AAW22999
ID AAW22999 standard; Protein: 364 AA.
XX
AC AAW22999;
XX
DT 20-FEB-1998 (first entry)
XX
DE Canine herpesvirus glycoprotein I PCG1364.
XX
KM Vaccine; vector; gene therapy; canid; dog; CHV; CgI; PCG1364;
XX
KW glycoprotein I.
XX
OS Canine herpesvirus.
XX
PN WO9729772-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US04115.
XX
PR 15-FEB-1996; 96US-0602010.
XX
PA (HESK-) HESKA CORP.
XX
PI Frank RA, Haanes EJ;
PI WPI; 1997-424758/39.
XX
DR N-PSDB; AAT75616.
XX
PT Recombinant canine herpes virus and its genome - useful as vaccine
PT to protect canids against infectious, metabolic or genetic diseases
XX
PS Claim 57; Page 181-182; 240pp; English.
XX
CC This protein comprises canine herpesvirus (CHV) glycoprotein I
CC (PCG1364). Its sequence was deduced from a coding region found in
CC CHV genomic DNA molecule ncu510592 (see AAT75616). PCG1364 can be
CC expressed in transformed host cells. CHV proteins, nucleic acids,
CC and antibodies raised against CHV proteins, can be used to protect
CC canids against CHV infection. Novel recombinant CHV and novel
CC recombinant CHV genomes that contain heterologous nucleic acid
CC molecules inserted e.g. into CgI gene, can be used as vaccines to
CC protect canids against infectious, metabolic or genetic diseases.
XX
SQ Sequence 364 AA:
Query Match 7.9%; Score 148; DB 18; Length 364;
Best Local Similarity 27.3%; Pred. No. 8.9e-06;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
4 LGLTALLAATLAPFGAMGIVITGNHVSARIDDDHIVYVAPRPEATIQQLFFMPCQ-R-P 62
16 LITLTMPLILFLFLYGVNGVYKGYISMLNTSSGFSIFPPDKFVSGRLFLDQHL 75
63 HKPVGSTVVAFAFRSDITNOCYOELSEEFENCNTHRSSVFCV--KVTEYFESASNRLLG 120
76 VNNSGCTIEFT--HFNNSCIVYQOTIEYFSCPRIFNNMFRSCGLKVSNNHESQRLINS 132
121 PPHPEKLTIRNPRPNDSGMFYVRLDDTKEPIDVFAIOLSVYQF 165
133 IENGVLLETINPKPNDSGVYFIRVQLENKK--TDVGIDAFIYSF 175
RESULT 7
AAW72659
ID AAW72659 standard; Protein: 364 AA.
XX
AC AAW72659;
XX

DT 07-JAN-1999 (first entry)
 XX Canine herpes virus protein sequence P0GI-364.
 DE
 XX
 KW Canine herpes virus; CHV; recombinant canine herpes virus vector;
 KW genome; vaccination; dog; protozoan; helminth; ectoparasite; bacteria;
 JW virus infection.
 XX
 OS Canine herpes virus.
 XX
 PN US5804197-A.
 XX
 PD 08-SEP-1998.
 XX
 PF 12-JUL-1996; 96US-0680726.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 15-FEB-1996; 96US-0602010.
 PR (HESK-) HESKA CORP.
 PI Frank RS, Haanes EJ;
 PI WPI: 1998-505590/43.
 DR N-PSDB: AAV6941.
 DR
 XX
 XX Canine herpes virus nucleic acids - useful for producing recombinant
 PT canine herpes virus vectors
 PS Claim 7; Column 133-136; 103pp; English.
 CC The present sequence represents a canine herpes virus (CHV) protein
 CC sequence. The nucleic acid sequence which encodes the protein can be
 CC used for DNA vaccination of dogs against CHV and also other infective
 CC agents such as protozoans, helminths, ectoparasites, bacteria and
 CC viruses. CHV can be formulated by incorporation of heterologous nucleic
 CC acid molecules as a single multivalent therapeutic composition against
 CC a variety of canine pathogens.
 CC
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 19; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 OY 4 LIGTIALAATLAPGANGIYITGNHVSARIDDDHIVYAPPEATTOLOLFMPGQR-P 62
 16 LITIMEPLIFLYGVNGFYKGTYSMFLNTSSGFSIFPDKFIYSGRLFLDDQHLS 75
 OY 63 HKPYSCTVRAFRSDITNOCYOELSEERFNCNTHRSSSVFVGC--KYTEYTFASNRLTG 120
 76 VNNISGTFIEFT--HNNSCITVQTEIEYSCPRIFNNAFRCLKVKSKHHESQLRINS 132
 DB 121 PPHPEKLTINRPNDSGMFYIVRLDTEPEIDVAIOLSYQF 165
 133 IENGVLLEITNRPNDSGVFIFRQLENNK--TDVGIPAFIYSF 175
 RESULT 8
 ID AAB51316 standard; Protein: 364 AA.
 AC AAB51316;
 XX
 DT 29-MAR-2001 (first entry)
 DE
 XX
 XX Canine herpes virus protein sequence SPO ID NO:56.
 KW Canine herpes virus; CHV; antiallergic; immunosuppressive; cytostatic;
 KW antibacterial; antiinflammatory; vaccine; candid; infectious disease;
 KW genetic disease; metabolic disease; abnormal; cell growth; allergy;
 KW degenerative process; immunological defect; autoimmune disease; cancer;
 KW cardiovascular disease; graft rejection; haematopoietic disorder;

KW immunodeficiency disease; immunoproliferative disease; septic shock;
 KW immunosuppressive disorder; inflammatory disease; jaundice.
 XX
 OS Canine herpes virus.
 XX
 PN US6159478-A.
 XX
 PD 12-DEC-2000.
 XX
 PF 29-JAN-1998; 98US-0092409.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 15-FEB-1996; 96US-0602010.
 PR (HESK-) HESKA CORP.
 PI Frank RS, Haanes EJ;
 PI WPI: 2001-090270/10.
 DR N-PSDB: AAF26761.
 DR
 XX
 XX Novel recombinant canine herpes virus protein useful for protecting
 PT animals, in particular candid from herpes virus infection and various
 PT diseases including cancer and autoimmune diseases
 PS Example 10; Column 135-136; 101pp; English.
 CC The present invention describes an isolated canine herpes virus (CHV)
 CC (I) CdutPase protein encoded by a CHV nucleic acid molecule that
 CC hybridises under stringent hybridisation conditions with the CdutPase
 CC gene. Also described is a therapeutic composition (II) comprising (I).
 CC (I) has antiallergic, immunosuppressive, cytostatic, antibacterial and
 CC antiinflammatory activities, and can be used in vaccines. (I) is useful
 CC for protecting an animal, in particular a candid from CHV. Therapeutic
 CC compositions comprising (I) are useful for treating infectious diseases,
 CC genetic diseases and other metabolic diseases, including diseases that
 CC lead to abnormal cell growth, degenerative processes and/or
 CC immunological defects, including allergies, autoimmune diseases,
 CC immunodeficiency diseases, graft rejection, haematopoietic
 CC disorders, cardiovascular diseases, graft rejection, haematopoietic
 CC disorders, immunodeficiency diseases, immunoproliferative diseases,
 CC immunosuppressive disorders, inflammatory diseases, jaundice, and septic
 CC shock. CHV need not be attenuated for use as a live vaccine vector due
 CC to the low pathogenicity of maternal CHV, particularly as compared to
 CC that of other herpesviruses. AAF26720 to AAF26786 and AAB51303 to
 CC AAB51327 represent CHV nucleotides, proteins and PCR primers used in the
 CC exemplification of the present invention.
 CC
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 22; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 OY 4 LIGTIALAATLAPGANGIYITGNHVSARIDDDHIVYAPPEATTOLOLFMPGQR-P 62
 16 LITIMEPLIFLYGVNGFYKGTYSMFLNTSSGFSIFPDKFIYSGRLFLDDQHLS 75
 DB 63 HKPYSCTVRAFRSDITNOCYOELSEERFNCNTHRSSSVFVGC--KYTEYTFASNRLTG 120
 76 VNNISGTFIEFT--HNNSCITVQTEIEYSCPRIFNNAFRCLKVKSKHHESQLRINS 132
 OY 121 PPHPEKLTINRPNDSGMFYIVRLDTEPEIDVAIOLSYQF 165
 133 IENGVLLEITNRPNDSGVFIFRQLENNK--TDVGIPAFIYSF 175
 RESULT 9
 ID AAF70645 standard; Protein: 350 AA.
 AC AAF70645;
 XX
 DT 29-APR-1991 (first entry)

```

XX DE Pseudorabies virus gp63 protein.
XX XX PRV; vaccine; GI: gp50; gp63.
XX OS Pseudorabies virus.
XX PN W08702058-A.
XX PD 09-APR-1987.
XX PE 28-AUG-1986; 86MO-US01761.
XX PR 16-JUL-1986; 86US-0886260.
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 26-MAR-1986; 86US-0844133.
XX PA (UPJO ) UPJOHN CO.
      (PETR/) PETROVSKIS E. A.
XX Petrovskis EA, Post LE, Timmlins JG;
DR WPI; 1987-108689/15.
DR N-PSDB; AAN70994.
XX Pseudo-rabies virus protein - produced from recombinant DNA and
PT used to produce vaccine and detect animals infected with virulent
XX virus.
XX PS Claim 8; Page 59; 67pp; English.
XX CC The PRV glycoprotein product may be used as in vaccination of
XX CC animals such as swine, sheep and goats against infection by the
XX CC virus. The protein may be produced from a transformed expression
XX CC system such as E. coli, yeast or CHO cells operatively linked to a
XX CC suitable expression control sequence. Glycoproteins gp1 and gp63 may
XX CC be used to distinguish between infected and vaccinated animals.
XX CC See also AAN70993-5.
XX SQ Sequence 350 AA;
Query Match 7.7%; Score 143.5; DB 8; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
QY 8 LALLAATLAPFGAM--GIYITGNHVSARIDDDHIVARPREATIQLOLFPMGQRPNK 65
  15 LLLAALTALALTPRVGVGLFRGAGSVHAGSAVLVPGDARNLTIDGTLFLLEGSPSN- 73
QY 66 YSGTVAVAFRSDITNOCYOLSEERFENCNTRSSVFVGC--KVTEYTFAS-----NRL 118
  74 YSGRVEL-LRLDPKRCACYTREYAEYDLCPRVHNEAFRCGLRRREPLARASAAVEARRL 132
DB 119 TGRPHFEKLTIRNRPDSMFYVIVRLDTPKRPIDVFAIQLSVYOFANPAATRG- 174
  133 -----LFSVRPAPRDAGSVLRAVNGT---TDLFVLTALV-----PRGRPNR 174
QY 175 --YSKASCRFTGLPTVQLEAYLRTESWRMMAVY--ATEATTSA-----EATPTPV 224
  175 TPSSADECR---PVV-----GSMHSLKLVVDPAEDAVFTTPRPIEPDPTTPAPR 221
DB 225 TATSAS-----ELEAEHFTFWLENGVDHYEPTPANENSNTVRLGMSPTLIGTV 277
  222 RGTGATPEPRSDDEEDE-----EGATTAATPVPGTLDANGTM--VLNASVSVLL 271
QY 278 AVVSATIG-----LVIVISITVTRMCTPRHKLRLDVVSODDERSSOTRRESRK 323
  272 AANMATAGARGPKIAMVLGPTIVLLIFLGVAACAARCAARGIASTGRDPGAARRSTR 331
DB RESULT 10

```

```

AAR63143
ID AAR63143 standard; Protein; 350 AA.
XX AAR63143;
AC AAR63143;
XX 12-JUN-1995 (first entry)
DT XX
XX glycoprotein 63 (gp63) of pseudorabies virus.
DE XX
XX pseudorabies virus; PRV; glycoprotein; gp50; GI: gp63;
XX determination; detection; vaccine; infected animal; isolation;
XX cloning; virulence.
XX OS Pseudorabies virus.
XX PN US5352575-A.
XX PD 04-OCT-1994.
XX PE 04-OCT-1985; 85US-0784787.
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 16-JUL-1986; 86US-0886260.
XX PR 29-JUN-1987; 87US-0100817.
XX PR 20-APR-1990; 90US-0513282.
XX PA (UPJO ) UPJOHN CO.
XX Petrovskis EA, Post LE, Timmlins JG;
XX PI WPI; 1994-316176/39.
XX DR N-PSDB; AAO73489.
XX XX
XX Identifying animals vaccinated against pseudorabies virus - by
PT detecting the absence of GI or GP.63 antibodies in serum to
PT distinguish vaccinated from infected animals
XX XX
XX Example 3; Column 21-24; 21pp; English.
XX CC AAR63143 shows the protein sequence of gp63 (glycoprotein) encoded by
XX CC AAO73489, isolated from Pseudorabies virus (PRV). The DNA and protein
XX CC sequences of the invention are useful in a method for distinguishing an
XX CC animal vaccinated with a PRV vaccine lacking glycoprotein GI, GP63 or
XX CC GP50 from an animal infected with a virulent wild-type PRV without
XX CC sacrificing the animal. The method is used to test animals such as
XX CC swine, cattle, sheep and goats. (see AAR63142 and AAR63144).
XX SQ Sequence 350 AA;
Query Match 7.7%; Score 143.5; DB 15; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
QY 8 LALLAATLAPFGAM--GIYITGNHVSARIDDDHIVARPREATIQLOLFPMGQRPNK 65
  15 LLLAALTALALTPRVGVGLFRGAGSVHAGSAVLVPGDARNLTIDGTLFLLEGSPSN- 73
DB 119 TGRPHFEKLTIRNRPDSMFYVIVRLDTPKRPIDVFAIQLSVYOFANPAATRG- 174
  133 -----LFSVRPAPRDAGSVLRAVNGT---TDLFVLTALV-----PRGRPNR 174
QY 175 --YSKASCRFTGLPTVQLEAYLRTESWRMMAVY--ATEATTSA-----EATPTPV 224
  175 TPSSADECR---PVV-----GSMHSLKLVVDPAEDAVFTTPRPIEPDPTTPAPR 221
DB 225 TATSAS-----ELEAEHFTFWLENGVDHYEPTPANENSNTVRLGMSPTLIGTV 277
  222 RGTGATPEPRSDDEEDE-----EGATTAATPVPGTLDANGTM--VLNASVSVLL 271
QY 278 AVVSATIG-----LVIVISITVTRMCTPRHKLRLDVVSODDERSSOTRRESRK 323
  272 AANMATAGARGPKIAMVLGPTIVLLIFLGVAACAARCAARGIASTGRDPGAARRSTR 331
DB RESULT 10

```

Db 222 RCGATPEPRDEEBDE-----EGATTAMTPVPQTLDANGTM---VLNASVYSRVLL 271

QY 278 AVVSATIG-----LVIVISIVTRNMCTPHRKLDTVSODDEERSQTRRESRK 323

Db 272 AANMTAGARGPKIAMVLGPTIVLLIFLGVCACARRCARGIASTGRDGAARRSTR 331

RESULT 11

AAE05396 standard; protein; 350 AA.

AAE05396:

24-SEP-2001 (first entry)

Pseudorabies virus (PRV) glycoprotein gp63.

Pseudorabies virus; PRV; glycoprotein; gp63; immunostimulant; vaccine;

PRV infection.

Pseudorabies virus.

Key Location/Qualifiers

Misc-difference 131 /note= "Encoded by GGG"

Misc-difference 132 /note= "Encoded by GTG"

Misc-difference 144 /note= "Encoded by CGG"

Misc-difference 207 /note= "Encoded by CGG"

Misc-difference 222 /note= "Encoded by GGG"

Misc-difference 223 /note= "Encoded by GGG"

Misc-difference 284 /note= "Encoded by CGG"

Misc-difference 334 /note= "Encoded by GCG"

Misc-difference 334 /note= "Encoded by GCG"

US6261563-B1.

17-JUL-2001.

07-JUN-1995; 95US-0485287.

20-APR-1990; 90US-0513282.

21-JUN-1994; 94US-0262813.

28-AUG-1986; 86MO-0501761.

26-NOV-1985; 85US-0801799.

26-MAR-1986; 86US-0844113.

16-JUL-1986; 86US-0886260.

29-JUN-1987; 87US-0100817.

(PHMA) PHARMACIA & UPJOHN CO.

Petrovskis EA, Post LE, Timmins JG;

WPI: 2001-450478/48.

N-PSDB; AAD10195.

polypeptide comprising a pure and isolated pseudorabies virus gp63

polypeptide or its fragments, useful as a vaccine for protecting

animals against pseudorabies virus infection -

Claim 1: Column 39-40; 21pp; English.

The invention relates to pseudorabies virus (PRV) glycoproteins gp50,

gp63, gI and their corresponding DNA molecules. These glycoproteins are

used as vaccines for protecting animals against PRV infection.

The invention also relates to methods for protecting animals against PRV

infections and methods for distinguishing between infected and vaccinated

animals. The present sequence is pseudorabies virus (PRV) glycoprotein

CC 9p63.

XX Sequence 350 AA;

SO Query Match 7.7%; Score 143.5; DB 22; Length 350;

Best Local Similarity 22.8%; Pred. No. 2.3e-05;

Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

QY 8 LALLAATLAFGAM--GIYIGNHYSARIDDDHIVAVRPPATIQLOLFMPGQRPHP 65

Db 15 LLLAATLALTPRGVGLFRGAGSVHAGSNAVLPDGAAPMLTIDGTLLEEGSPSPN- 73

QY 66 YSGIVRAVFRSDITNOCIOELSEFRNCITRRSSVFGC--KYETEFSSAS-----NRL 118

Db 74 YSGIVEL-LRLDPRACCTRYETAAEYDLCPRVHHEAFRCGLKRPDLARRASAAVEARLL 132

QY 119 TGPHPFKLTIRPNRDSGMFTYVIRLDOTKEPIYFAIQLSYQFANTATRGL----- 174

Db 133 -----LFVSRPAPDAGSYLVLRVNGT--TDLEVITALLY-----PPRGRRHP 174

QY 175 --YSKASCTFFGLPTVQLEAYLRTESNRNMQAVY--ATEATTTS-----AEATPTPV 224

Db 175 TPSSADECR---PVV-----GSMHDSLRYVDPADPAVFTTPPIEPPTTPAP 221

QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPTLIQTV 277

Db 222 RCGATPEPRDEEBDE-----EGATTAMTPVPQTLDANGTM---VLNASVYSRVLL 271

QY 278 AVVSATIG-----LVIVISIVTRNMCTPHRKLDTVSODDEERSQTRRESRK 323

Db 272 AANMTAGARGPKIAMVLGPTIVLLIFLGVCACARRCARGIASTGRDGAARRSTR 331

RESULT 12

AAE0637 standard; protein; 317 AA.

AAE0637:

21-DEC-1995 (first entry)

Bovine herpes virus-1 mutant ORF1 product.

BVH-1; vaccine; gIV gene; antigen.

Bovine herpesvirus.

EP63403-A1.

19-JUL-1995.

18-NOV-1994; 94EP-0203361.

23-NOV-1993; 93EP-0203274.

(ALKU) AKZO NOBEL NV.

Keil G;

WPI: 1995-247499/33.

N-PSDB; AAO99001.

New bovine herpes virus with mutation in ORF1 and polyA signal for

gIV gene useful as a vaccine, esp. where the mutation is insertion

of sequence encoding an heterologous antigen

Claim 2: Page 13-14; 28pp; English.

To produce a new BVH-1 mutant, DNA encoding gIV (flanked on both

sides by a sequence that allows homologous recombination) and a

genotypically neg. BVH-1 (or its DNA) is introduced into a host

cell. Since the gIV-neg. virus cannot replicate, virus particles

are produced only when homologous recombination with the DNA has

CC occurred to restore the giv-pos. phenotype. The mutant is used
 CC for (multivalent) vaccine manufacture.
 XX
 SQ Sequence 317 AA;

Query Match 7.7%; Score 143; DB 16; Length 317;
 Best Local Similarity 27.0%; Pred. No. 2.2e-05;
 Matches 68; Conservative 35; Mismatches 123; Indels 26; Gaps 12;

QY 1 MASLGLTALIAATLAFPGAMGIVITGNHVSARIDDIHIVAPREPTIQL--QLFEMP 58
 DB 1 MRRLLLMNVLLAARAP--ARSLVREGAVGLADGVAAVAP--IDATIALGRLIFLE 57
 QY 59 GARP-HKPYSGTVAVAFRSDITNOCYOELSEERFENCNHRSSVFVGCVTETFSASNR 117
 DB 58 HQLPAGRRYNGTVEL--LRHYAGDCFVMLQDTAFASCPVANDAFRCLHADTRPARSER 116
 QY 118 LTGP--PHPKLTIRNRPDNGMFYIVRL----DDTKETIVFAQLSVQFAN---- 167
 DB 117 RASAAVENHVLFSIARRPRIDSLYFLRVGIYGTAGSERRRVFPPLAATVHSGEGDP 176
 DB 168 --TAATRGLYS--KASCRFGLPVTOLEAVLRTESWRNQAVYA--TEATTSAEATTP 222
 DB 177 EAAAHKPGTVEAVANCER--GLDASSASLY---DAAIAAPPAAGATTGPTASSEGAAT 232
 QY 223 PVTATSALELA 234
 DB 233 PERVEDTEVEA 244

RESULT 13

AAU04970
 ID AAU04970 standard; Protein; 350 AA.

AC AAU04970;
 DT 26-SEP-2001 (first entry)

DE Pseudorabies virus glycoprotein 63, gp63.

KM Glycoprotein 63; gp63; immunogen; vaccine; PRV; Bulbar paralysis;
 KM Aujeszky's disease; mad itch.

OS Pseudorabies virus.

FX Key Location/Qualifiers

FT Misc-difference 117 /note= "Encoded by GAG"

FT Misc-difference 229 /note= "Encoded by GAG"

FT Misc-difference 232 /note= "Encoded by GAG"

PN US6251634-B1.

PD 26-JUN-2001.

PE 07-JUN-1995; 950S-0485290.

PR 20-APR-1990; 900S-0513282.

PR 28-AUG-1986; 86MO-US01761.

PR 26-NOV-1985; 85US-0801799.

PR 26-MAR-1986; 86US-0844113.

PR 16-JUL-1986; 86US-0886260.

PR 29-JUN-1987; 87US-0100817.

PA (PHMA) PHARMACIA & UPJOHN CO.
 PI Petrovskis EA, Post LE, Timmins JG;
 DR WPI; 2001-431968/46.
 DR N-PSDB; AAS08831.
 XX

PT New recombinant DNA molecules encoding a polypeptide displaying
 PT pseudorabies virus (PRV) gp63 antigenicity, useful for screening
 PT animals to determine whether they are infected with PRV -
 XX
 PS Claim 1; Column 40; 23pp; English.

CC The sequence is the pseudorabies virus (PRV) glycoprotein 63. The
 CC invention relates to isolated recombinant DNA molecules, which encode a
 CC polypeptide displaying pseudorabies virus (PRV) gp63 antigenicity.
 CC The DNA sequences are useful for screening animals to determine
 CC whether they are infected with PRV and also for expressing the
 CC glycoproteins encoded. The DNA sequences are also useful in producing
 CC glycoprotein gp63, which may be used as vaccines for protecting animals
 CC against PRV infection, variously called Bulbar paralysis, Aujeszky's
 CC disease or mad itch. PRV infects a wide range of animals and birds and
 CC is invariably fatal.

SQ Sequence 350 AA;

Query Match 7.6%; Score 142.5; DB 22; Length 350;
 Best Local Similarity 22.1%; Pred. No. 2.9e-05;
 Matches 80; Conservative 42; Mismatches 149; Indels 91; Gaps 16;

QY 8 LALLAATLAFPGAM--GIYITGNHVSARIDDIHIVAPREPTIQLQLFEMPQORPHK 65
 DB 15 LLLAALTALALTRPVGVGLRAGAVSVHAGSAVLVPGDAPNLTIGTLFLFEGPSPSN 73
 QY 66 YSGTVAVAFRSDITNOCYOELSEERFENCNHRSSVFVGCVTETFSASNRITGP---- 121
 DB 74 YSGRVEL-LRLDPKRCACYTEYAAEYDLCPRVHHEAFRGL-----RRGPLARR 122
 QY 122 ----PHPKLTIRNRPDNGMFYIVRLDDTKETIVFAQLSVQFANTATRGL-- 174
 DB 123 ASAAVEARLLFVSRRPAPDAGSYLVLRVNGT--TDLEVLALV-----PRGRPH 172
 QY 175 ----YKASCRFGLPVTOLEAVLRTESWRNQAVY--ATEATTTS-----AEATTP 222
 DB 173 HPTPSSADECR---PVY-----GSHWDSLRVVDPAEDAVFTTPPIEPPPTPA 219
 QY 223 PVTATSALELA-----ELEAEHFTFPMLENGVDHYEPTPANENSNVVRIGTMSPTLIGVT 275
 DB 220 PPRGTGATPPGRSDDEEED-----EGATVTAMTVPPTGLDANGM---VLNAAVSVR 269
 QY 276 VAAVVSATIG-----LVIVISIVTRNCTPHRKLDIVSODEERSQTRRES 321
 DB 270 LLAANAATGARGRKIAMVLGPTIVLILFLGVCACARCARCAGIAGTGRDGAARRST 329
 QY 322 RK 323
 DB 330 RR 331

RESULT 14

AAB82502
 ID AAB82502 standard; Protein; 350 AA.

AC AAB82502;

DT 05-SEP-2001 (first entry)

DE Pseudorabies virus glycoprotein gp63.

KM PRV; glycoprotein; gp50; vaccine; diagnosis.

OS Pseudorabies virus.

FX Key Location/Qualifiers

FT Misc-difference 79 /note= "encoded by GAG"

FT Misc-difference 229 /note= "encoded by GAG"

PN US6255078-B1.

```

XX 03-JUL-2001.
PD
XX
XX 07-JUN-1995; 95US-0485289.
XX
XX 20-APR-1990; 90US-0513282.
XX 21-JUN-1994; 94US-0262813.
XX 28-AUG-1986; 86US-0501761.
XX 26-MAR-1986; 86US-0844113.
XX 16-JUL-1986; 86US-0886260.
XX 29-JUN-1987; 87US-0100817.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Petrovskis EA, Post LE, Timmins JG;
XX
XX WPI: 2001-432046/46.
XX
XX N-PSDB; AAF90626.
XX
XX New recombinant DNA for screening animals actively infected with
XX pseudorabies virus (PRV), or for producing proteins useful as a vaccine
XX for protecting animals against PRV infection
XX
XX Example 3; Column 21-24; 21pp; English.
XX
XX The present sequence is that of pseudorabies virus (PRV)
XX glycoprotein gp63. The invention provides PRV gp50, gp63 and gI
XX glycoproteins (see A482501-03) and polynucleotides (see
XX AAF90623-27), and transformed host cells (especially CHO, yeast
XX and Escherichia coli) used to produce the polypeptides. Also
XX provided are subunit vaccines for PRV, methods for protecting
XX animals against PRV infection and methods for distinguishing
XX between infected and vaccinated animals. Commercial vaccine PRVs
XX have been found to have the gI and gp63 genes deleted. The gI and
XX gp63 polypeptides can therefore be used as diagnostic agents to
XX distinguish between animals vaccinated with these commercial
XX vaccines and those infected with the virulent virus.
XX
XX Sequence 350 AA;
XX
XX Query Match 7.6%; Score 141.5; DB 22; Length 350;
XX Best Local Similarity 22.8%; Pred. No. 3.7e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX 8 LALLAATLAPGAM--GIVITGNHVSARIDDDHIVYAPREATIOLQLFPMGGRPKR 65
XX 15 LLLAALTLAALPRYGCVLFRGAASVHVAGSAVLPGDANLITDGLFLGSPSPN- 73
XX 66 YSGTVAVAFRSDITNOCYOELESEERENCTHSSSVFGC--KYTEYTFAS-----NRL 118
XX 74 YSGRVGL-LRDPKRACTTREVAAETDLCPRVHNEAFNGCLRKREPLARRASAAVARRL 132
XX 119 TGPPEFKLITRNPRPNDSCMFYIVRLDTEKEPIDVAIOLSYOFANTATRGL---- 174
XX 133 -----LEVSRPAPPAGSYVLARVNGT--TDLVLTALV-----PPGRPHHP 174
XX 175 --YSKASCTFGLPTVQLEAVLRTESMRNMOAYV--ATEATTS-----AEATTPPV 224
XX 175 TPSSADECK---PVY-----GSMHDSLRVVDPAEDVFTTPPIPEPEPTPAP 221
XX 225 TATSAS-----ELEAEHFTFMLENGVDHETTPAENSNTVRLGTSPTLIGTVA 277
XX 222 RGTGATPPGRSDEEDE-----EGATTAMTPVPGGLDANGTM--VINASVVSRYVL 271
XX 278 AVVSATIG-----LVIVISIVTFNMCTPRKIDTYSODEERSOTREESRK 323
XX 272 AAAMATAGARGKIAVLGPTIVLLIFLGVCACARRCARGIASTGRDPCGARRSTRR 331
XX
XX RESULT 15
XX AAR48063
XX ID AAR48063 standard; Protein; 380 AA.

```

```

AC AAR48063;
XX
XX 20-JUL-1994 (first entry)
XX
XX Sequence of polypeptide encoded by the first open reading frame in
XX the unique short (us) region of bovine herpes virus (BHV) genome.
XX
XX Insertion region; unique short region; Us; vaccine; antigen.
XX
XX Bovine herpes virus type 1, strain ST.
XX
XX MO9400586-A.
XX
XX 06-JAN-1994.
XX
XX 25-JUN-1993; 93MO-FR00642.
XX
XX 26-JUN-1992; 92FR-0007930.
XX
XX (INMR ) RHONE MERIEUX SA.
XX
XX Audonnet JF, Legasteleis ICMA, Leung-tack P, Riviere MEA;
XX
XX WPI: 1994-02622/03.
XX
XX N-PSDB; AA033350.
XX
XX New insertion region sequence of bovine herpes virus genomic DNA
XX used for recombinant virus with this region deleted or
XX inactivated; useful in vaccines allowing differentiation between
XX vaccinated and infected cattle
XX
XX Claim 9; Fig 2; 47pp; French.
XX
XX The 4190 bp sequence in AA055350 encodes polypeptides homologous to
XX HSV-1 gI, gE and US9; these are neither essential for in vitro
XX replication nor important in inducing a protective immune response.
XX It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
XX known as infectious bovine rhinotracheitis virus.) The sequence
XX forms the insertion region in genomic DNA. rBHV in which the
XX specific insertion region, esp. nucleotides 172-1311, has been
XX deleted or inactivated by insertion are claimed.
XX
XX Sequence 380 AA;
XX
XX Query Match 7.5%; Score 140.5; DB 15; Length 380;
XX Best Local Similarity 25.3%; Pred. No. 5.2e-05;
XX Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
XX
XX 1 MASLIGTLLAATLAPGAMGIVITGNHVSARIDDDHIVYAPREATIOLQLFPM 58
XX 1 MRCLLMAYVLAARAP--ARSIVRGAVGLADPVAFAVHP--TDATLALRKLITLE 57
XX 59 GQRP-HKPTSGIVYAFRSDITNOCYOELESEERENCTHSSSVFGCKYETTFASNR 117
XX 58 HQLPAGRRNGIVEL-LRIHAAGDFVWLQTTAFASCPRVANNARRSCLADTRPARSER 116
XX 118 LTGP--PHPEKLTITRNPRPNDSCMFYIVRL--DTEKEPIDVAIOLSYOFA----- 166
XX 117 RASAAVENHVLFSIARPRIDSGLYELRVAVIYGTAGSERRRDVPLAAEFHSGEGDD 176
XX 167 -----NTATRGLYSKASCTFGL-----PTVQLEAVLRTESMR 201
XX 177 EAARTPPARSRPASPGLSSASLDRALARSPOAPPAPARRAARAPRPERVDE 236
XX 202 NMQAVYATEATTSAEATTPPVATAS 230
XX 237 TTEVEAATRAGSAPALTTTPAGPTASPA 265
XX
XX Search completed: May 5, 2003, 16:12:58
XX Job time : 56.5 secs

```

THIS PAGE BLANK (USPTO)

~~BEST AVAILABLE COPY~~

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:11:13 ; Search time 19.5 Seconds
(Without alignments)
546,210 Million cell updates/sec

Title: US-09-993-777-68

Sequence: 1 MASLGLTALLAATLAPGANGI...VELVAIVNPSALSSPSISIKW 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCrus.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1863	100.0	362	5	PCT-US96-03916-7
2	1863	100.0	362	5	Sequence 7, Appl
3	1863	100.0	362	5	Sequence 68, Appl
4	1863	100.0	362	5	Sequence 28, Appl
5	1863	100.0	362	5	Sequence 25, Appl
6	1863	100.0	362	5	Sequence 2, Appl
7	1863	100.0	362	5	Sequence 36, Appl
8	1863	100.0	362	5	Sequence 8, Appl
9	1863	100.0	362	5	Sequence 19, Appl
10	1863	100.0	362	5	Sequence 1, Appl
11	1863	100.0	362	5	Sequence 1, Appl
12	1863	100.0	362	5	Sequence 1, Appl
13	1863	100.0	362	5	Sequence 1, Appl
14	1863	100.0	362	5	Sequence 1, Appl
15	1863	100.0	362	5	Sequence 1, Appl
16	1863	100.0	362	5	Sequence 1, Appl
17	1863	100.0	362	5	Sequence 1, Appl
18	1863	100.0	362	5	Sequence 1, Appl
19	1863	100.0	362	5	Sequence 1, Appl
20	1863	100.0	362	5	Sequence 1, Appl
21	1863	100.0	362	5	Sequence 1, Appl
22	1863	100.0	362	5	Sequence 1, Appl
23	1863	100.0	362	5	Sequence 1, Appl
24	1863	100.0	362	5	Sequence 1, Appl
25	1863	100.0	362	5	Sequence 1, Appl
26	1863	100.0	362	5	Sequence 1, Appl
27	1863	100.0	362	5	Sequence 1, Appl

28	93.5	5.0	907	3	US-08-783-774-2	Sequence 2, Appl
29	93.5	5.0	907	4	US-09-328-599A-1	Sequence 1, Appl
30	93.5	5.0	907	5	PCT-US95-04611A-19	Sequence 19, Appl
31	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl
32	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl
33	92.5	5.0	547	1	US-08-433-010-1	Sequence 1, Appl
34	92.5	5.0	547	1	US-08-482-882-1	Sequence 1, Appl
35	92.5	5.0	547	1	US-08-483-589-1	Sequence 1, Appl
36	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
37	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
38	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
39	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
40	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
41	92.5	5.0	547	3	US-08-714-017-1	Sequence 1, Appl
42	92.5	5.0	547	3	US-08-714-017-1	Sequence 1, Appl
43	92.5	5.0	547	3	US-08-714-017-1	Sequence 1, Appl
44	92.5	5.0	547	4	US-08-714-017-1	Sequence 1, Appl
45	90.5	4.9	518	4	US-09-591-435-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
PCT-US96-03916-7
Sequence 7, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: COCHIN, Mark A.
TITLE OF INVENTION: RECOMBINANT INFECTIONS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
PCT-US96-03916-7
Query Match 100.0%; Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MASLGLTALLAATLAPGANGIIVTGNHVSARIDDDHIVAPRPATIDOLFMPQ 60
1 MASLGLTALLAATLAPGANGIIVTGNHVSARIDDDHIVAPRPATIDOLFMPQ 60

QY 61 RPHKPSGTVAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFASNRLTG 120
DB 61 RPHKPSGTVAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFASNRLTG 120
QY 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
DB 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
QY 181 RTFGLPTVOLEAVLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
DB 181 RTFGLPTVOLEAVLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGVIVISITRMKCTP 300
DB 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGVIVISITRMKCTP 300
QY 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADODELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADODELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 2

PCT-US96-03916-68

; Sequence 68, Application PC/TUS9603916

; GENERAL INFORMATION:

; APPLICANT: Wild, Martha A.

; APPLICANT: Cochran, Mark D.

; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS

; TITLE OF INVENTION: AND USES THEREOF

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/03916

; FILING DATE: 23-MAR-1995

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/126,597

; FILING DATE: 24-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 39116-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 362 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US96-03916-68

QY 1 MASILGTLALIAATLAPFGAMGIVITGNHVSARIIDDHIVAVPREATIQQLFFMPGQ 60
DB 1 MASILGTLALIAATLAPFGAMGIVITGNHVSARIIDDHIVAVPREATIQQLFFMPGQ 60
QY 61 RPHKPSGTVAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFASNRLTG 120
DB 61 RPHKPSGTVAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFASNRLTG 120
QY 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
DB 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
QY 181 RTFGLPTVOLEAVLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
DB 181 RTFGLPTVOLEAVLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGVIVISITRMKCTP 300
DB 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGVIVISITRMKCTP 300
QY 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADODELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADODELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 3

US-08-709-731A-28

; Sequence 28, Application US/08709731A

; Patent No. 6322780

; GENERAL INFORMATION:

; APPLICANT: Lee, Lucy F.

; APPLICANT: Mazerian, Keyvan

; APPLICANT: Witter, Richard L.

; APPLICANT: Wu, Ping

; TITLE OF INVENTION: Marek's Disease Virus Genes and Their

; TITLE OF INVENTION: Use in Vaccines for Protection Against Marek's Disease

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Birch, Stewart, Kolasch and Birch, LLP

; STREET: P.O. Box 747

; CITY: Falls Church

; STATE: VA

; COUNTRY: US

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/709,731A

; FILING DATE: 05-JUL-1996

; CLASSIFICATION: 424

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/499,474

; FILING DATE: 07-JULY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Murphy Jr., Gerald M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 1644-110FPC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 205-8000

; TELEFAX: (703) 205-8050

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Marek's disease virus type I
 STRAIN: GA
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..355
 OTHER INFORMATION: /label=protein
 OTHER INFORMATION: /note="g1 protein"
 US-08-709-731A-28

Query Match 8.2% Score 152; DB 4; Length 355;
 Best Local Similarity 22.9%; Pred. No. 1.2e-07;
 Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;

19 GAGGIVTGNHVSARIDDDHIVAPRPE-ATLOLEFMPGQPHKPYSGTVRVAFRSD 77
 15 GIMSVITGTVLSTDSALVAFGCLDKAVNRQGLFLDQRTSSYTGTEI-LKMD 73
 78 ITNOCYOELESEERFENCTHRSSVFVGCCKVTEYTSASRLTGPSPHK---LTINRPP 134
 74 EBYKCVSLHATSYMCDPAIDATVRCGRDAVVAOPHDKV--QPFKGTLLRIYEPV 131
 135 NDSGMFYVIRLDTRKEPIDVFAIOLSVQFANTAFRTGLSKASCRTGLPVOLEAVL 194
 132 SDTGSYIRVVALAG--RNMSDIFRMAVIRG-----SKWACHSASSFOAHKCI 179
 195 RTEE--SMRMQAVYVTEATTPTPVATTSASELEAEHETFPWLENGVDHYEPT 252
 180 RYVDRMAFENVYLIGHGNLSDSELAHYNITPOSIS--TDINITTPEYDNGSTIYSP 238
 253 P---ANENSVTVRLGT-MSPLIGTVAAV--SATIGLVIV--ISIVTRNCKTPHK 303
 239 VENLFNNHSHVDAMNSTGMMNTVLTLYPLRIYFSIMYICIAIALIYVCEKCRSPHR 298
 304 LDTVSDDEESQTRRESKRFQPMVACEINKGADQDSEIVE 344
 299 I----YIGEPKRSDE-----APLITSAVNESFQYDVNVE 328

RESULT 4
 US-08-344-833-2
 Sequence 2, 5874280
 Patent No. 5874280
 GENERAL INFORMATION:
 APPLICANT: Kell, G other
 TITLE OF INVENTION: Recombinant Bovine Herpesvirus
 TITLE OF INVENTION: Vaccine
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Organon Teknika Corporation
 STREET: 1330-A Piccard Drive
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,833
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Blackstone, William B.
 REGISTRATION NUMBER: 29,772
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 258-5200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-344-833-2

Query Match 7.9% Score 148; DB 2; Length 317;
 Best Local Similarity 27.1%; Pred. No. 2.7e-07;
 Matches 68; Conservative 34; Mismatches 125; Indels 24; Gaps 11;

1 MASLIGTLALATLAPFGAMGIVITGNHVSARIDDDHIVAPRPEATLOL-OLEFMP 58
 1 MRLLIMVVAALAAAP--ARSLVIGEAIVGLADGVAAVAPR-IDATLALRGLTLE 57
 59 GQRP-HKPYSGTVRVAFRSDITNOCYOELESEERFENCTHRSSVFVGCCKVTEYTSASNR 117
 58 HOLPAGRRYNGTVEL-LRYHAAGDCEVWLOTATFASCPVANDAFSCIAADTRABSER 116
 118 LTGP--PHPEKLTIRNRPNDGMEYIVRL---DITKEPIDVFAIOLSVQFAN---- 167
 117 RASAVERNHLFSLARPRPIDSGLVFLRGVIGTAGSERRRDVFPLAFVHSFGEPODP 176
 168 --TAATRGLYS--KASCRTGLPVOLEAVLPTESWRMNOAVYATBATTSNATPTP 223
 177 EAAAHPTGVEAVEARCR-GLDASSASLYDRALAAPGAA--TTPGPTASSGGAATP 233
 224 VTATSAELEA 234
 234 ERVDETTEVEA 244

RESULT 5
 US-08-680-726A-56
 Sequence 56, Application US/08680726A
 Patent No. 580167
 GENERAL INFORMATION:
 APPLICANT: Haanes, Elizabeth J.
 APPLICANT: Frank, Rexann S.
 TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
 NUMBER OF SEQUENCES: 92
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/680,726A
 FILING DATE: 12-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Coonell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-46-C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-680-726A-56

Query Match 7.98; Score 148; DB 1; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

Qy 4 LIGTLALLAATLAPFGAMGIYITGNHVSARIDDDHIVAPREPTQLOLFFMPGQR-P 62
Db 16 LLITMPLPLFLPLXNGVYKGTYSIMPLNTSSGFSIFPDDKFIYSGRLFLDDQHL 75

Qy 63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEFGC--KYLETFSASNRLTG 120
Db 76 VNNVSGTIEFT--HNNSCITVOTIEYFSCPRIFNNAFSCIAKYSKHHSQDLRINS 132

Qy 121 PPHEFKLTIRNPNRNSGMFYIVRLDTPKEPIDVFAIQLSVYOF 165
Db 133 IENGVLLEITNPKRNDGCVYFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 6
US-09-092-409-56
Sequence 56, Application US/09092409
Patent No. 6159478

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-092-409-56

Query Match 7.98; Score 148; DB 4; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

Qy 4 LIGTLALLAATLAPFGAMGIYITGNHVSARIDDDHIVAPREPTQLOLFFMPGQR-P 62
Db 16 LLITMPLPLFLPLXNGVYKGTYSIMPLNTSSGFSIFPDDKFIYSGRLFLDDQHL 75

Qy 63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEFGC--KYLETFSASNRLTG 120
Db 76 VNNVSGTIEFT--HNNSCITVOTIEYFSCPRIFNNAFSCIAKYSKHHSQDLRINS 132

Qy 121 PPHEFKLTIRNPNRNSGMFYIVRLDTPKEPIDVFAIQLSVYOF 165
Db 133 IENGVLLEITNPKRNDGCVYFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 7
US-08-911-321-10
Sequence 10, Application US/08911321
Patent No. 6010703

GENERAL INFORMATION:

APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Poxvirus
TITLE OF INVENTION: Vaccine Against
TITLE OF INVENTION: Feline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096,183
FILING DATE: July 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: NO. 6010703e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 370
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Polypeptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORGANISM SOURCE:
ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: Deduced Sequence
OTHER INFORMATION: 91
US-08-911-321-10

Query Match 7.88; Score 145; DB 3; Length 370;
Best Local Similarity 22.08; Pred. No. 7.1e-07;
Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

Qy 5 LIGTLALLAATLAPFGAMGIYITGNHVSARIDDDHIVAPRE-ARTQLOLFFMPGQ-RP 62
Db 1 MSSIAFIYILMAIGTYGIVYRGDHSIHYDTSAGFYITLTLENFTLYGHLFLDDQRLP 60

[illegible]

RESULT 8
 5352575-7
 Patent No. 5352575
 APPLICANT: PETROWSKIS, ERIK A.; POST, LEONARD E.; TIMMINS, JAMES G.
 TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
 NUMBER OF SEQUENCES: 12
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/513, 282
 FILING DATE: 20-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 100, 817
 FILING DATE: 29-JUN-1987
 APPLICATION NUMBER: 886, 260
 FILING DATE: 16-JUL-1986
 APPLICATION NUMBER: 784, 787
 FILING DATE: 04-OCT-1985
 APPLICATION NUMBER: 801, 799
 FILING DATE: 26-NOV-1985
 APPLICATION NUMBER: 844, 113
 FILING DATE: 26-MAR-1986
 SEQ ID NO.: 7
 LENGTH: 350

Query Match	7.78;	Score 143.5;	DB 6;	Length 350;
Best Local Similarity	22.88;	Pred. No. 9.3e-07;		
Matches 82;	Conservative 42;	Mismatches 149;	Indels 87;	Gaps 17;

```

QY 8 LALATLAPPGAM--GIVTGNHNSARIDDDHIVAPREGATLOLOTFPMQGRPKR 65
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 15 LLAALTLAALTPRVGSVLPECGAAVSVMVGSVAVLPCGDANLITDSTLTLEGPSPN- 73
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 YSGTVAVPNSDITNOCUYELSEERFCKNSTRSSVFCG--KTEYTFEGAS-----NRL 118
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 74 YSGRVEL-LRDPFRACQYTRREVALEYDCLSPVHNHEAFRCCLKEPRLAPRASAAVEARL 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 TGRPHFKLTIRNRPDMSGFVYVRLDTPKEPIVAFIOLSYOAPAAATRGL--- 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 133 -----LFSRRAPRPDASVYLKRVNCG---TDLFVLTAIV-----PRGRGPHR 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 175 --YSKASCTPCLPTVOLLEYLTBEESRMOQAAV--ATEATTS-----AEATPRV 224
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 175 TPSSADECR-----PV-----GSMHDLKRVPRADAVFTTPRIEPEPRTTAPR 221
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 225 TATSAS-----ELEAHTFPMLENGVDHETPTANENSNVYVRLGTSPILGIVVA 277
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 222 RGTATPERSDEEEDB-----EGATLAMPYVOTIDANGIN--VLMASVSVRL 271
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 278 AVSAATIG-----LYVIVSYVRNMCYTPHKRLDYSODDERESTOTREERK 322
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 272 AANAATGARGPCKTAMVLTPTVLLFLGVCACARCKACAGINSTGRDGAARSTR 333
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 9
 US-08-924-345-2
 Sequence 2, Application US/08924345
 Patent No. 6224878
 GENERAL INFORMATION:
 APPLICANT: LEUNG-YACK Patricia
 APPLICANT: LEGASTELLOIS Isabelle, Christine, Marie-Andree
 APPLICANT: AUDONNET Jean-Christophe, Francis
 APPLICANT: RIVIERE Michel, Emile, Albert
 TITLE OF INVENTION: Mutants and vaccines of the Infectious
 TITLE OF INVENTION: Bovine Rhinotracheitis virus
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LARSON AND TAYLOR
 STREET: 727 SOUTH TWENTY-THIRD STREET
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (Epo)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,345
 FILING DATE: 04-SEP-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/199,172
 FILING DATE: 09-AUG-1994
 APPLICATION NUMBER: FR 92 07930
 FILING DATE: 26-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: SARRO, THOMAS P.
 REGISTRATION NUMBER: 19396
 REFERENCE/DOCKET NUMBER: XI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 920-7200
 TELEFAX: (703) 892-6428
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 380 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match	7.54;	Score 140.5;	DB 4;	length 380;
Best Local Similarity	25.38;	Pred. No. 2,76-06;		
Matches	68;	Conservative	33;	Mismatches 125; Indels 43; Gaps
QY	1 MASLLGTLAALATAPGANGIYITGNHYSARIDDDIIVYAPREPTIOL--GLFMP	58		
DB	1 MRCLLLMVYLLARAP--ASLVYRGEAVGLRACPAFVHP--IDATLALRGLIFLE	57		
QY	59 GQRP-HKPSYSGIYRAFSRSDITNOCYQELSEREFENCRHSSSVFGCVYETFSASNR	117		
DB	58 HOLPAGRRYGVYEL--LRHAAGCGFMLOTTAFSCRYVANNFRSLHADIPTPARSER	116		
QY	118 LTGP--PHPKLTINRPNDSCMFYIVYL-----DHPKEIDVFAIOLSYQFA-----	166		
DB	117 RASAAYENHVLFSIARPRIDISGLFIRAGVIYGTGASGERRDVFLPAFVHSVEPDGP	176		
QY	167 -----NTATKGLYKSKSCITFL-----PIYQLETLAFTEESMR	201		
DB	177 EAAAFTPAPSRQSRPASGLTSSASLYDLRLANSPQAPPPRAPPRAARAAGRRPREVDE	236		
QY	202 NMQAVATEYVETITTSAEATITPPYATAS	230		
DB	237 TTEVDAATKRGSAFALITTPACPTTSPAA	265		

Page 7

```

FLYING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
FAX: (202) 887-1500
INFORMATION FOR SRD ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLGY: unknown
MOLECULE TYPE: protein
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUPL, Fig. 46
US-08-473-089-63

Query Match          5.8%; Score 108; DB 4; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016; 89; Indels 46; Gaps 11;
Matches 62; Conservative 30; Mismatches 6;

OY      60 QRPKPFYSCTRYAVAFRSDDITNOCYOFELSEREFENCIRHSSVYGCKYLETFFS-----AS 115
DB      86 QRHQHQAISLTVOOOOQOOOQOOOQOHLOOQO-QOLAAASAVFPAQOPATTSATAPMA 144
OY      116 NRTGPHPEFKLITRNPRNDSGMFYIVRLDTKEPI-----D 154
DB      145 NTTGSPSAF--PVQASRPNLYVS---QLPTTLTPVSSNNQOOLPQOLQQOOLQO 197
OY      155 VFALQSVYQFANTAGLYSKASCRTGLPTVOL-EAYLTDESRRNQAVY----A 208
DB      198 QPPQVSVAPLNTAING---SPFSKETTLTVSAPESTLKETEPENNNTKINDTGA 254
OY      209 TEATTTSAEAT--TTPVTATASELEAEHTFPMLENGVDHYEPPT 253
DB      255 TTAATTTATETEIKRKEADTPAS-LHDHYLVPNQR-AHNSKPID 299

RESULT 14
US-08-487-072A-63
Sequence 63, Application US/08487072A
Patent No 6421684
GENERAL INFORMATION:
Applicant: Mochly-Rosen, Daria
Applicant: Ron, Dorit
Title of Invention: MD-40 - Derived Peptides and Uses
Title of Invention: Theroef
Number of Sequences: 205
Correspondence Address:
Addressee: Morrison & Foerster
Street: 2000 Pennsylvania Avenue, NW
City: Washington
State: DC
Country: USA
Zip: 20006-1812
COMPUTER READABLE FORM:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
Application Number: US/08/487,072A
Filing Date: 07-JUN-1995
Classification: 514
Attorney/Agent Information:
Name: MURASHIGE, KATE H.
Registration Number: 29,959
Reference/Docket Number: 2550-0025.20
Telecommunication Information:

```

```

OY 209 T E A T T S A E A T - T P P V A T S A S E A E H F T P P M L E N G D V D H E P T 253
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 255 T T A T T T T A T E T E I K P R E D A T P A S - L H Q D H Y L V P Y N Q R - A N H S K P I P 259

```

Search completed: May 5, 2003, 16:16:02
 Job time : 20.5 secs

```
Search completed: May 5, 2003, 16:16:02
Job time : 20.5 secs
```

```

OY 209 TEATTTSSEAT--TTPPVVATSSSELEAEHPTPLMGVDHYEPTP 253
    | | | | | : | | | | | : | | | | | : | | | | |
Db 255 TTAATTTTATETLKKPREDATPRAS-LHQDHYLVLPYNGR-ANHSKRP 259

```

Search completed: May 5, 2003, 16:16:02
 Job time : 20.5 secs

```
Search completed: May 5, 2003, 16:16:02
Job time : 20.5 secs
```

```
Search completed: May 5, 2003, 16:16:02
Job time : 20.5 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:09:18 ; Search time 15.5 Seconds
(Without alignments)
2245.204 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863

Sequence: 1 MASULGTLALLATAPRGA.....VELVAIVNPSALSPDSIKM 362

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	164	8.8	420	2	T42616	envelope protein -
2	162.5	8.7	354	1	VG8B67	glycoprotein D pre
3	155	8.3	353	1	C66113	glycoprotein D pre
4	153.5	8.2	424	1	VG8B63	glycoprotein gp63
5	143.5	7.7	350	2	VG8B63	glycoprotein I - b
6	140.5	7.5	380	2	S53785	glycoprotein I - t
7	125	6.7	356	2	U02352	probable glycoprot
8	124.5	6.7	683	2	T03146	probable glycoprot
9	115	6.2	457	1	RW8574	glycoprotein I pre
10	113.5	6.1	390	1	Q08E77	glycoprotein I pre
11	111.5	6.0	149	2	A61162	hypothetical prote
12	108.5	5.8	355	2	C39725	WD-40 repeat I pre
13	108	5.8	713	2	JN0133	glycoprotein I pre
14	107	5.7	372	2	Q08E88	glycoprotein I pre
15	99	5.3	372	2	F43674	US7 protein - hma
16	99	5.3	1036	2	S73601	protein P200 - Myc
17	98.5	5.3	1140	2	S73786	hypothetical prote
18	98	5.3	503	2	B38745	cell adhesion mole
19	98	5.3	507	2	S64507	probable membrane
20	97	5.2	1220	2	S48387	SLM1 protein - yea
21	96.5	5.2	814	1	A39752	fibroblast growth
22	95.5	5.1	797	1	VG8E61	glycoprotein X pre
23	95.5	5.1	867	2	T45463	membrane glycoprot
24	95	5.1	1777	2	T34369	hypothetical prote
25	94	5.0	796	2	T21460	hypothetical prote
26	93.5	5.0	645	2	T29818	hypothetical prote
27	93.5	5.0	907	1	Q08E21	membrane antigen g
28	93.5	5.0	3020	2	A43932	mucin 2 precursor
29	93	5.0	1051	2	S55259	TfPI1 protein - mou

30	92.5	5.0	1778	2	AF1116	internal protein
31	92	4.9	1044	2	E95375	probable drug resi
32	91.5	4.9	510	2	T47374	hypothetical prote
33	91	4.9	365	2	A34424	CD44 membrane gly
34	91	4.9	836	2	S49940	cell division cont
35	90.5	4.9	547	1	S28904	intercellular adhe
36	90.5	4.9	785	2	T37329	probable oligopept
37	90.5	4.9	786	2	T19017	hypothetical prote
38	90.5	4.9	1429	2	T41699	hypothetical prote
39	90	4.8	233	2	C84193	hypothetical prote
40	90	4.8	788	2	T34248	hypothetical prote
41	89.5	4.8	826	2	G90283	hypothetical prote
42	89.5	4.8	866	2	T45462	membrane glycoprot
43	89.5	4.8	992	2	T38817	hypothetical prote
44	89	4.8	629	2	A15155	probable peptidogl
45	89	4.8	678	2	S54308	DNA binding protei

ALIGNMENTS

RESULT 1	T42616	envelope protein - equine herpesvirus 4 (strain NS80567)
C:Species:	equine herpesvirus 4	
A:Variate:	strain NS80567	
C:Date:	11-Jan-2000	#sequence=revision 11-Jan-2000 #text-change 21-Jul-2000
C:Accession:	T42616	
R:RefSeq:	E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.	
J:Gen:	Virol. 79, 1197-1203, 1998	
A:Title:	The DNA sequence of equine herpesvirus-4.	
A:Reference number:	222173; PMID:98264497; PMID:9603335	
A:Accession:	T42616	
A:Status:	preliminary: translated from GB/EMBL/DDAJ	
A:Molecule type:	DNA	
A:Residues:	1-420 <TEU>	
A:Cross-reference:	EMBL:AF030027; NID:92605950; PIDN:AAC59593.1; PID:92606021	
A:Experimental source:	strain NS80567	
C:Genetics:		
A:Note:	73	
C:Superfamily:	pseudotables virus glycoprotein gp63	
Query Match	8.84; Score 164; DB 2; Length 420;	
Best Local Similarity	25.58; Pred No. 9.6e-06;	
Matches	96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;	
OY	10 LLAATLAPRGAAGIYITGNHVSANIDDDHIVYARPPATLQ-LPFEMROR-PKRPYS 67	
DB	13 LLAISMCM--ATAIYKGEHMSMTLNSSFAVYRKOKSLVVGHMFLDGOGLPTNTYS 69	
OY	68 GTVAFAFRSDITNOCYOELESEERENCTHRSSSVYGC--KYTEFTSASNRLTGPHPF 125	
DB	70 GLIEL-TIHNYSGCYVIGTISTESCPRVANNAFSCLAHTSNHNDYHVTSEYIN 128	
OY	126 KLTIRNRPDSCGMEYIVIRLDTRKPIDVFAIQLSVYOF-ANRAIRGLXKASGRTFG 184	
DB	129 LLNITRPOPDSGAVYLRKYLHNA-PTADVGSAFVYDLOSNVPEPVPAKEPSNFT 187	
OY	185 LPTVOLFAVIRTEESWRNQAIVATEATTSAEAT--TPPVYATSASELEAHTFPW 241	
DB	188 RTPAPAPANSTK-----TGSNTTSSOSTWLYPTP-----RRA 221	
OY	242 LKNGVDHDEPTANEN--SNVTVRL-----GTMSPF-----LIGVVAVVSATIG----- 285	
DB	222 LET---LHTTAPANETVSGDYAMCHGFRPSAVPTIYMLLGLT-----GALPE 269	
OY	286 --LIVYISYITRNMCYPRKRLDTVS-----ODDEERSQTRRSR-KFGPVN-----ACEIN 333	
DB	270 DVLLEDESELK--TPPKPQTSRTSGEDGFKQTSNTPSKSRNKKIVAMVVIPTACVLM 326	
OY	334 KGADDSTVETVAIVN 350	
DB	327 -----LLIVYGAIIIN 337	

RESULT 2

glycoprotein D precursor - human herpesvirus 3
 VGBE67

N:Alternate names: glycoprotein IV

C:Species: human herpesvirus 3, varicella-zoster virus

C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999

C:Accession: F27345

R:Davidson, A.J.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A:Title: The complete DNA sequence of varicella-zoster virus.

A:Reference number: A27345; MUID:86306657; PMID:3018124

A:Accession: F27345

A:Molecule type: DNA

A:Residues: 1-354 <DAV>

A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27950.1; PID:g60056

C:Genetics:

A:Gene: 67

C:Superfamily: herpesvirus glycoprotein D

Keywords: glycoprotein; phosphoprotein; transmembrane protein

-17/Domain: signal sequence #status predicted <SIG>

-18-354/Product: glycoprotein D #status predicted <GPD>

F:33,47,67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted.

Query Match 8.7%; Score 162.5; DB 1; Length 354;

Best Local Similarity 22.4%; Pred. No. 1e-05;

Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

QY 23 IYTGHHVSARIDDDHIVAPRPE--ATIQQLFPMGQRP-HKPYSGTVNARSDI 78

DB 21 LIFGQGVSLQVNSLSLILPMQNDNYTEIKQLVFIQGLPTGNYSGTELELY-ADT 79

QY 79 TNCQYQELSEERENCTHRSSEVFGCKV--EYTFSSNRLTGPHPKLTIRNRP 135

DB 80 VAFCSFVSQVIRIDGCPRTTSAFISCRKXKSHNIGNSDRISTEPAGYMLTTPRGIN 139

QY 136 DSGMFYVIRLDDTKEPIDVFAIQLSVY-----OPANTATRGYSKAS 179

DB 140 DAGVYVLLVLDHSRS-TDGFILGVNVYTGSHHNIHGVIYTPSLONGYSTALFQQA- 197

QY 180 CRFGGLPT-----VLEAVLRTEES-KRNQAVYVTEATTTSAEKTTPRPV 225

DB 198 -RCDLPAPRPGSGTSLFQHMLDLRAGKSLIEDNPMWLH-EDVVTETKRSVKEG----- 248

QY 226 ATSASELEAEHFTFWLENCVDHYEPTPAN-----NVTYRLGTMSPTLIGTV 276

DB 249 -----IEN---HYPTDMSTLPEKSLNDPPELLT-----IIPVA 281

DB 277 AAVVSATIGLVIVISIVTRNM 297

DB 282 SVMILTAMVIVIVSVKRRRI 302

RESULT 3

C66113

glycoprotein D precursor - cercopithecine herpesvirus 9 (strain DHV)

N:Alternate names: membrane glycoprotein 1

C:Species: cercopithecine herpesvirus 9

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: C66113

R:Fletcher III, T.M.; Gray, W.L.

Virol. 193, 762-773, 1993

A:Title: DNA sequence and genetic organization of the unique short (Us) region of the s

A:Reference number: A66113; MUID:93212509; PMID:8384754

A:Accession: C66113

A:Molecule type: DNA

A:Residues: 1-353 <FLE>

A:Cross-references: GB:I07067; NID:g310715; PIDN:AAA7888.1; PID:g310718

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-353/Product: glycoprotein D #status predicted <GPD>

F:275-293/Domain: transmembrane #status predicted <TMN>

F:40,75,84,122,138,227,252/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 8.3%; Score 155; DB 1; Length 353;

Best Local Similarity 20.2%; Pred. No. 4.2e-05;

Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY 18 FG---AMGIVITGNHVSARIDDD--HIVYAPPEATIQQLFPMGQRP-HKPYSGTV 71

DB 20 FGIQCAAIIRGNISILVYNSATSIFLKGNNNDASIRGRFLFGDQFVTVNTVNTVE 79

QY 72 VAFRSITNOCYQELSEERENCTHRSSEVFGCKV--TEYTSASNRLTGPHPKLTIR 130

DB 80 L-LHVQTLTCLQPLRYVMGECPRIRTCALICRVKRSWHYENATQDTPRNEIIFKMN 138

QY 131 NRPNDSCMPYVIRLDDTKEPIDVFAIQLSVYQFNTATRLYKASCRTEGLTFYOL 190

DB 139 NTKVEDAGIYLLVVDLYT-SLFDIFVSLNVPKQDTSMEDVY-----PPVYS 188

QY 191 EAV-LTTEESMRNQAVVATEATTSAEATTPPVATTSASELEAEHFTFWLENCVDHY 249

DB 189 PSHILMTFKCHFPVHNGEOSILQHIY-----SDVDTEENLSMGKDLGSR 238

QY 250 EPTPANENSVTVRL-----GTMSPTLIGTVAAVVSATIGLVIVISI-VTRNMC 298

DB 239 QKPRKNFNPDKVNVTHETKRLMESSADVFMIAVITASLIVLIIIVVGIYRRRS 298

QY 299 TPRKIDTVSQDDEERSQTRRE 320

DB 299 SEKRKIYRPRKREQASTERE 320

RESULT 4

VGBE69

glycoprotein gp63 precursor - equine herpesvirus 1

N:Alternate names: glycoprotein I precursor; hypothetical 46k protein; ORF2 protein

C:Species: equine herpesvirus 1

A:Note: host Equus caballus (domestic horse)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: C36646; J00998; A36803

R:Anderson, J.C.; Winslow, J.; Allen, G.; Paoletti, E.

J. Gen. Virol. 71, 2969-2978, 1990

A:Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with h

A:Reference number: A36646; MUID:91108393; PMID:2177089

A:Accession: C36646

A:Molecule type: DNA

A:Residues: 1-424 <AUD>

A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Kentucky D

R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.

Gene 101, 203-208, 1991

A:Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesvir

A:Reference number: J00998; MUID:91276272; PMID:1647359

A:Accession: J00998

A:Molecule type: DNA

A:Residues: 1-424 <ELT>

A:Cross-references: GB:M36299; NID:g330787; PIDN:AAA6547.1; PID:g330788

R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

submitted to GenBank, March 1992

A:Description: The DNA sequence of equine herpesvirus-1.

A:Reference number: A36803

A:Accession: A36803

A:Molecule type: DNA

A:Residues: 1-424 <TEL>

A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Ab4p

R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

Virol. 189, 304-316, 1992

A:Title: The DNA sequence of equine herpesvirus-1.

A:Reference number: A41831; MUID:92295566; PMID:1318606

A:Contents: annotation, possible protein-coding frames

A:Note: neither amino acid nor nucleotide sequence is given

C:Genetics:
 A:Gene: 73
 C:Superfamily: pseudorabies virus glycoprotein gp63
 C:Keywords: glycoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-424/Product: glycoprotein gp63 #status predicted <MNT>
 F:320-336/Domain: transmembrane #status predicted <TM1>
 F:35,67,78,121,131,236,307/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
 Best Local Similarity 23.8%; Score 153.5; DB 1; Length 424;
 Matches 70; Conservative 41; Mismatches 126; Indels 57; Gaps 12;

OY 1 MASLGLTLALATLAPFGAMGIVITGNHVSARIDDDHIVIVAPREPAITOL-QLFEMP 59
 DB 1 MAKLTGMFSAAILLSMAICSTAIYRGHSMYLNASSEFAYPTDQSLVLGHLFLD 60
 OY 60 QR-PHKYSGTVRAFRSDITNOCYOLSEERFENCTHRSSSVFVC-KVETYSASN 116
 DB 61 QRLPTNYSGLIEL-IHYNSSVCYVLOTISYESCPVANNARSCLEKTHHDFR 119
 OY 117 RLTPPHPEKLTIRNRPDSCMFYIVRLDTPKEIDYFAIOLSYQFANTATRGIX 176
 DB 120 VNASVETNVLNITRPPDTSAGAILKLDHA-PRADYGVSAFYIDL- 167
 OY 177 KASCTFEGLEPTVQ---LEAVLTRESWRMOAYATATTS---AEATPPVATSA 229
 DB 168 KSKTVPDPMTQVTEPTSTVSTPYDITDVTETESTISIQOAMSTQTP-SATWG 226
 OY 230 SELEAEHFTPEMLNGVDHYEPTPANENSVYRIG-----TMSPTL 271
 DB 227 TQLTTE-----LPTNE---TVIQEALCHMFQSTSTVPL 260

RESULT 5
 VEB63
 glycoprotein gp63 - suid herpesvirus 1
 C:Species: suid herpesvirus 1
 A:Note: host Sus scrofa domestica (domestic pig)
 C:Date: 31-Mar-1986 #sequence_revision 31-Mar-1986 #text_change 16-Jul-1999
 C:Accession: A29012
 R:Petkovskis, E.A.; Timmings, J.G.; Post, L.E.
 J. Virol. 60, 185-193, 1986
 A:Title: Use of lambda phage to isolate genes for two pseudorabies virus glycoproteins w
 A:Reference number: A29012; MUID:86308235; PMID:3018284
 A:Molecule type: DNA
 A:Residues: 1-350 <P>
 A:Cross-references: GB:M14336; NID:9334055; PIDN:AAC35204.1; PID:9334056
 A:Experimental source: strain Rice
 A:Superfamily: pseudorabies virus glycoprotein gp63
 C:Keywords: glycoprotein; transmembrane protein
 F:11-72/Domain: transmembrane #status predicted <TM1>
 F:286-308/Domain: transmembrane #status predicted <TM2>
 F:56,73,153,256,262,275/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
 Best Local Similarity 7.7%; Score 143.5; DB 1; Length 350;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

OY 8 LALLATLAPFGAM-GIVITGNHVSARIDDDHIVIVAPREPAITOLQLFEMPGRPKP 65
 DB 15 LLLALTLALTLPRVGVLFRRGAGVAVHAGAVLVGDAPNLITIGTLLEFGSPEN- 73
 OY 66 YSGTVRAFRSDITNOCYOLSEERFENCTHRSSSVFVC-KVETYSASN-NRL 118
 DB 74 YSGRVEL-LRLDPRKACYTREVAAYELCPRVHHAFFGCLRRREPLARASAAVEARL 132
 OY 119 TGPPIHFKLTIRNRPDSCMFYIVRLDTPKEIDYFAIOLSYQFANTATRG- 174
 DB 133 -----LFVSRPAPDPAGSYLVLRVAVNGT---TDLEVLALAV-----PPRRPHHP 174
 OY 175 --YSKASCTFEGLEPTVQLEAVLTRESWRMOAYV-ATEATTS-----AEATPPV 224

DB 175 TPSSADECR-----PVV-----GSHWDLRLVDPADAVFTTPPIEPEPTTPAP 221
 OY 225 TATSSA-----ELAEHFTPEMLNGVDHYEPTPANENSVYRIGTMSPTLIGVTA 277
 DB 222 ROTGATPPRPSDEEDE-----EGATTAMPVPCITLDANGTM---VLNASVSVLL 271
 OY 278 AVASATIG-----LVIVISIVRNKCTPRKLDVSOQDEERSQTRRESRK 323
 DB 272 AANNTAARPGKIAMVGLGPTIVLILFLGVCACARRCARGISTGRDGAARSTR 331

RESULT 6
 S35785
 glycoprotein I - bovine herpesvirus 1
 C:Species: bovine herpesvirus 1
 C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 24-Nov-1999
 C:Accession: S35785
 R:Audonnet, J.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35782
 A:Accession: S35785
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <AND>
 A:Cross-references: EMBL:223068; NID:9312185; PIDN:CAA80605.1; PID:9312189
 C:Keywords: glycoprotein

Query Match
 Best Local Similarity 7.3%; Score 140.5; DB 2; Length 380;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;

OY 1 MASLGLTLALATLAPFGAMGIVITGNHVSARIDDDHIVIVAPREPAITOL-QLFEMP 58
 DB 1 MRCLLMVAVLAARAAP--ARSLVYRGKENGALRAGPVAFVAPND-TNIALALGRILIE 57
 OY 59 GQRP-HKPYSGTVRAFRSDITNOCYOLSEERFENCTHRSSSVFVCCKTETESASNR 117
 DB 58 HQLPAGRRNGVTEL-LRYHAAGDCEFWLCTTAFSCPRVANNARFSCLAADRPRRSR 116
 OY 118 LTGP-PHPKLTIRNRPDSCMFYIVRLDTPKEIDYFAIOLSYQFA----- 166
 DB 117 RASAAVENHVLFSIARPRIDSGLYFLRGVITGTSERRRDFPLAATVHSGEPDP 176
 OY 167 -----NTAATRGLYSKASCTFGL-----PYQLEAVLTRESWR 201
 DB 177 EAARFPAPRSKOSRPAASLTSSALYDRALASPPAPRPAPRAAAGRRPRRYDE 236
 OY 202 NWQAYVATEATTTSATATTPPTVATSA 230
 DB 237 TTEVAATRAGSAFALTTPPAGPTASPA 265

RESULT 7
 J02352
 glycoprotein I - turkey herpesvirus
 N:Alternate names: ORF 7 protein
 C:Species: turkey herpesvirus
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
 C:Accession: J02352
 R:Genik, V.; Bartel, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ro
 J. Gen. Virol. 74, 2151-2162, 1993
 A:Title: The complete sequence and gene organization of the short unique region of he
 A:Reference number: J02352; MUID:9401999; PMID:8409940
 A:Accession: J02352
 A:Molecule type: DNA
 A:Residues: 1-356 <ZEL>
 C:Keywords: glycoprotein; transmembrane protein
 F:5-21/Domain: transmembrane #status predicted <TM1>
 F:277-293/Domain: transmembrane #status predicted <TM2>
 F:154,167,230,260/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.7%; Score 125; DB 2; Length 356;
 Best Local Similarity 22.2%; Pred. No. 0.012;
 Matches 85; Conservative 54; Mismatches 174; Indels 70; Gaps 17;

QY 6 GTLALLATLAPF-----GAGGIYITGNHVSARIDDD-HYIVAPRPATITQLOLFEMPG 60
 DB 5 GIACMCVTLILFCIIKTCOMYRGSLVSTYDQSAQIFGIDIVNVNKGKLFMGDQ 64
 QY 61 RPKPYSGTVAVAFRSDITNOCYOLSEEFNCTHRSSVFCCKYTEFASNRITG 120
 DB 65 YLEIYSCTMEI-LKMNQARCYSIATATYACPIISSYFRCRAVYTRHSI-- 121
 QY 121 PPHF-----FKLITRNPDSGMEFYVRLDTEPIDVFAIQLSYQFANTATRG 175
 DB 122 --HPOYNGLLITIEPRMDSGIYRTSIDGPNKS-----DYARTSIFCNG 168
 QY 176 SKASCRF-----FELPIVQ--LEAYLRTESSRMN-----QAYVATEITTSANT 220
 DB 169 SSGSCSNPROKVDKMCIPVNRNIAFERVYLTLLHVGRLPYGDLTLQOTRKMTT--APT 225
 QY 221 PTVATASASELAEHFTFMLENGVDHYEPTPANENSNTVRLGTSPTLIGTVAAV 280
 DB 226 YRIRRTVEGLLTKTSPDIDLNMTNL-PLPI---SNT---DYMSVIMRRVALRIRY 278
 QY 281 SATIGLYIVISYTRNMCTPHRKLDIVSODDEBSQTRRSKFG--PMVACETINKAQ 338
 DB 279 AYLVIALIALLIVT--VCSAHRK-----GSCSRRRRIYIGNEPTLTSTINGNFQ 326
 QY 339 DSELVELVAIVNPSALSSPSIK 361
 DB 327 EKETKNV-----FSDISDAELLE 344

RESULT 8

T03146
 probable glycoprotein A8 - alcelaphine herpesvirus 1
 C:Species: alcelaphine herpesvirus 1
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
 C:Accession: T03146
 J. Ensser, A.; Pfanz, R.; Fleckenstein, B.
 J. Virol. 71, 6517-6525, 1997
 A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
 A:Reference number: 214840; MID:97404659; PMID:9261371
 A:Accession: T03146
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-683 <ENS>
 A:Cross-references: EMBL:AF005370; NID:92337967; PIDN:AA058098.1; PID:92338014

Query Match 6.7%; Score 124.5; DB 2; Length 683;
 Best Local Similarity 21.9%; Pred. No. 0.032;
 Matches 72; Conservative 46; Mismatches 108; Indels 103; Gaps 14;

QY 11 LAATLAPFGMAGIYITGNHVSARIDDDHYIVAPRP--ATITQLOLFEMPGPHKRYSG 68
 DB 341 ITATISPRGKIKAVNTGNF--SRNANISLAFLSKCKEYAGVLIQA-FEESTRP---PG 394
 QY 69 TVAVAFRSDITNOCYOLSEEFNCTHRSSVFCCKYTEFASNRITLGPHPFKLT 128
 DB 395 TVAPGILSTJAN-----FETSTNKSPPYT-----PPPAKISTPPGLNLT 435
 QY 129 IRRPRRDSMGFYVIRLDTEPIDVFAIQLSYQFANTATRGLSKASC----- 180
 DB 436 LITAGEHNSG-----IGSTLEPLTVSVQVLOTSPSPRDSITVYIKLITVPDOKIV 488
 QY 181 -----RTFGPLTVQLEAYLRTESSRMNQAIVATTEATTSABAATPPVATASSEL 232
 DB 489 SPGLVTPGKSTLPISVMTFHSREGSSPK-----POTPAKTSSEASLPLLT 538
 QY 233 EAEHFTFMLENGVDHYEPTPAN-----ENSNTV-----RLGTSPTLIGV 274
 DB 539 -----PIPTNTEKSGSRTFASSTVSVDTFTFGDDVNTVGTMSPS---I 577

QY 275 TVAAVSATIGLYIVISYTRNMCTPHRK 303
 DB 578 TQTLPIRPTSGROYIV-----GCCTLNR 602

RESULT 9

RMSST4
 T-cell surface glycoprotein CD4 precursor - mouse
 N:Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen T4/Len
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
 R:Tourville, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R.
 Science 234, 610-614, 1986
 A:Title: Isolation and sequence of L3T4 complementary DNA clones: expression in T cell
 A:Reference number: A02110; MID:87018845; PMID:3094146
 A:Accession: A02110
 A:Molecule type: mRNA
 A:Residues: 1-457 <TOU>
 A:Cross-references: GB:M13816; NID:9192070; PIDN:AAA37267.1; PID:9309112
 R:Litman, D.R.; Gettner, S.N.
 Nature 325, 453-455, 1987
 A:Title: Unusual intron in the immunoglobulin domain of the newly isolated murine CD4
 A:Reference number: A26038; MID:87115821; PMID:3027575
 A:Accession: A26038
 A:Molecule type: mRNA
 A:Residues: 1-457 <LIT>
 A:Cross-references: GB:X04836; NID:950353; PIDN:CAA28539.1; PID:950354
 R:Gorman, S.D.; Tourville, B.; Parnes, J.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
 A:Title: Structure of the mouse gene encoding CD4 and an unusual transcript in brain.
 A:Reference number: A39893; MID:88041159; PMID:2823269
 A:Accession: A39893
 A:Molecule type: DNA
 A:Residues: 1-25, 'E', 27-457 <GOR>
 A:Cross-references: GB:M17080; GB:J03003; NID:9192515; PIDN:AAA37402.1; PID:9387124
 R:Maddon, P.J.; Molineux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey, M.; Alt, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
 A:Title: Structure and expression of the human and mouse T4 genes.
 A:Reference number: A39955; MID:88097446; PMID:3501122
 A:Accession: A39955
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 25-457 <MAD>
 A:Note: the cited Genbank accession number, J03564, is not in release 101.0
 R:Parnes, J.R.; Hunkapiller, T.
 Immunol. Rev. 100, 109-127, 1987
 A:Title: L3T4 and the immunoglobulin gene superfamily: New relationships between the
 A:Reference number: I54564; MID:88152875; PMID:3326818
 A:Accession: I54564
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-457 <RES>
 A:Cross-references: GB:M36850; NID:9198670; PIDN:AAA94401.1; PID:9198671
 A:Accession: I69018
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 208-318 <RE2>
 A:Cross-references: GB:M36851; NID:9198672; PIDN:AAA39402.1; PID:9554183
 R:Classon, B.J.; Tsagaratos, J.; Kirsztbaum, L.; Maddox, J.; Mackay, C.R.; Brandon, M.
 Immunogenetics 23, 129-132, 1986
 A:Title: The L3T4 antigen in mouse and the sheep equivalet are immunoglobulin-like.
 A:Reference number: A47642; MID:86166694; PMID:3082751
 A:Accession: A47642
 A:Molecule type: protein
 A:Residues: 27-43 <CLA>
 C:Comment: This protein is expressed on most thymocytes, on a subset of mature T-cell
 C:Genetics:
 A:introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
 C:Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
 C:Keywords: alternative initiators; duplication; immunoglobulin; T-cell; transmembrane
 F1-26; Domain: signal sequence; status predicted <SIG>
 F127-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>

```

F:35-114/Domain: immunoglobulin homology <IM>
F:139-190/Domain: immunoglobulin homology <status atypical <IM2>
F:220-301/Domain: immunoglobulin homology <IM3>
F:241-457/Product: CD4, brain-specific short form #status predicted <BRA>
F:321-377/Domain: immunoglobulin homology <IM4>
F:395-419/Domain: transmembrane #status predicted <TM>
F:420-457/Domain: intracellular #status predicted <INT>
F:42-112,159-188,328-370/Disulfide bonds: #status predicted
F:187,298,333,392/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match      6.2% Score 115; DB 1; Length 457;
Best Local Similarity 20.6% Pred. No. 0.11;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

QY 19 GAMGIYVITGNHVSARIDDDHIVAPREATTIQLQF--PMGQRFHKYSGTYVAVR 75
Db 93 GFSPILIT--NKLKEDSDQTYICELENRE--EVELMEFKVTSFPGSLQOSLITLSDN 149
      | : : : |
76 SDITNOCYQELSEERFENCTHRSSVFGCKVTEYTFSSNRLTGPPHPRKLIIRNPN 135
      | : : : |
150 SVKSN---PLTF--CKHKKGKVGSGSV-----LMSLRQ 181
      | : : : |
QY 136 DSGMEYIVIRLDITKEPIDVAIQLSVYQFANPAATRGLYSKASCRITFGIPLYQLEAYLR 195
Db 182 DSDFNKCTVTLLDQK--NMFKTLISVGFQSTAIR--AKSGESAEPFLNFAE----- 233
QY 196 TEESWRN--WQAYVATEATTTSSEATPTTPVATSSASELAEHFTFFPLENGDHYEPP 253
Db 234 -ENGDELIMKA-----KSFQPMPISTIKNEVSV 265
      | : : : |
QY 254 ANENSVTVRLGTMSPLLCGYVAAVVNTIGLYIVISTVNMCTPRKRIIDYQSDDBE 313
Db 266 QKSTDKLQIKLETLPLTLKIPVSLQTRGSGNL---ILITDKETLHQEVNLVYKKAQ 321
QY 314 RSOTRRESRKFGPVACEIN-----KADDO---SELVELVAIVPSK----- 353
Db 322 LNNFT-----LICEVNGPSPKMKLTLKQNOARVSEQKVVGYVAPEFGIMQCT 371
      | : : : |
QY 354 LSSPDSIKM 362
Db 372 LSEGDKVKA 380

RESULT 10
QOBE77
glycoprotein 1 precursor - human herpesvirus 1 (strain 17)
Species: human herpesvirus 1
Note: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
Accession: A05243
KMGCSCHD.D.J.: Dolan, A.; Donald, S.; Rixon, F.J.
F:1 Mol Biol 181, 1-13, 1985
F:1 File: Sequence determination and genetic content of the short unique region
A: Reference number: A00656; MUID:85160822; PMID:2984429
A: Accession: A05243
A: Molecule type: DNA
A: Residues: 1-390 <CMCG>
A: Cross-references: GB:100036; NID:9291490; PIDN:AAA96681.1; PID:9291497
C: Genetics:
A: Gene: US7
C: Superfamily: herpesvirus US7 protein
C: Keywords: glycoprotein; transmembrane protein
F:1-33/Domain: signal sequence #status predicted <SIG>
F:124-390/Product: glycoprotein 1 #status predicted <GPI>
F:127-293/Domain: transmembrane #status predicted <TM>
F:156,175,257/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match      6.1% Score 113.5; DB 1; Length 390;
Best Local Similarity 20.8% Pred. No. 0.12;
Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;

7 TLAIATATLAPFAMCAGIVTGNHVSARIDDDHIVAPREATTIQLQFPMGQRFHKP- 65
      | : : : |

```

[illegible]


```
QY 167 NTAAATRGLYSKASCRTEGLPTVQLEAYLRTESMNMQAVVATEATTSAEATPPVTA 226
      |||
      |||
Db 169 NGTFVYNGSDYGCDPAQLP-----FSAPRLGSSVYTPGASRPPTPT 212
      |||
QY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSNVTVRIGTMSPTLIGVTVAAVVSATIGL 286
      |||
      |||
Db 213 TTSPSPRPDPPTPAPG-----DTGTPAPASGERAPPNSTRSASBSRHLTVAGVIOIAIPA 267
      |||
QY 287 VIVISIVTRN-MCTPHRKLDTVSQDDEERSQTRRESRKFGP-WVACEINKGA 336
      |||
      |||
Db 268 SIIAFVFLGSCICFIHRC-----QRRYRRPGQIYNPGVSCAVNEAA 310
      |||
```

RESULT 15

F43674
US7 protein - human herpesvirus 2 (strain H52)

C:/Species: human herpesvirus 2

Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999

Accession: F43674

MGeoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C.

J. Gen. Virol. 68, 19-38, 1987

A:Title: DNA sequence and genetic content of the HindIII 1 region in the short unique c
utionary comparisons.

A:Reference number: A43674; MUID:87111457; PMID:3027242

A:Accession: F43674

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <MCG>

A:Cross-references: EMBL:X04798; NID:g55900; PIDN:CAA28485.1; PID:g55906

C:Superfamily: herpesvirus US7 protein

Query Match 5.3%; Score 99; DB 2; Length 372;

Best local similarity 21.0%; Pred No. 1.8;

Matches 74; Conservative 49; Mismatches 165; Indels 64; Gaps 13;

```
QY 3 SLGTTLAATLAATLAPFGMGIVITGNHSARIDDDHIVAPREAITOL-----OLEF 56
      |||
      |||
Db 5 SLQG-LATIGLWVC---ATGLVVRGPTVSL-VSDSLVAGAVGQGFVEDLAVRGELHF 59
      |||
QY 57 MGOORPHKPYSGIVAVAFRSDINOCYOLSEPERENCTHSSSVFVGCXVETXPSASN 116
      |||
      |||
Db 60 VCAQVPHNTYIDGIIELFPHLGNHCPRVVHVYTLACPRPAVAFTLCRSTHHS---116
      |||
QY 117 RLTGPPHP-----KLTRNPRNDGSMFYIVRLDP-TKEPIDVFAIOLSYQFA 166
      |||
      |||
Db 117 ----PAYPTLEGLAROPDLVRKTRATRDYAGLYLRLVWGSATNASRFVLGVALS--A 168
      |||
      |||
QY 167 NTAAATRGLYSKASCRTEGLPTVQLEAYLRTESMNMQAVVATEATTSAEATPPVTA 226
      |||
      |||
Db 169 NGTFVYNGSDYGCDPAQLP-----FSAPRLGSSVYTPGASRPPTPT 212
      |||
QY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSNVTVRIGTMSPTLIGVTVAAVVSATIGL 286
      |||
      |||
Db 213 TTSPSPRPDPPTPAPG-----DTGTPAPASGEIAPPNSTRSASBSRHLTVAGVIOIAIPA 267
      |||
QY 287 VIVISIVTRN-MCTPHRKLDTVSQDDEERSQTRRESRKFGP-WVACEINKGA 336
      |||
      |||
Db 268 SIIAFVFLGSCICFIHRC-----QRRYRRPGQIYNPGVSCAVNEAA 310
      |||
```

Search completed: May 5, 2003, 16:15:17

Job time : 17.5 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:06:38 ; Search time 15.5 Seconds
(Without alignments)
968.673 Million cell updates/sec

Title: US-09-993-777-68

Perfected score: 1863
Sequence: 1 MASLGTALLAATLAPFGA.....VELVALVNPALSPPDSIKM 362

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.5	8.7	354	1	VGLI_VZVD
2	155	8.3	353	1	VGLI_SYVD
3	153.5	8.2	424	1	VGLI_HSEVB
4	143.5	7.7	350	1	VGLI_PSVRI
5	140.5	7.5	380	1	VGLI_HSVBS
6	115	6.2	457	1	CD4_MOUSE
7	113.5	6.1	390	1	VGLI_HSV11
8	108	5.8	713	1	TUPI_YEAST
9	107	5.7	372	1	VGLI_HSV23
10	99	5.3	1036	1	VGLI_HSV2H
11	98.5	5.3	1140	1	P200_MYCPN
12	98	5.3	503	1	CD4_KAT
13	98	5.3	507	1	IG46_TENST
14	98	5.3	1220	1	SLN1_TENST
15	97	5.2	797	1	VGLX_HSEVB
16	95.5	5.1	907	1	VGP3_EBV
17	93.5	5.0	1051	1	TF1A_MOUSE
18	91	4.9	836	1	NOT3_YEAST
19	91	4.9	3178	1	YS89_CABEL
20	90.5	4.9	547	1	IC43_HUMAN
21	90.5	4.9	785	1	CP7A_CABEL
22	90.5	4.9	1429	1	YC31_SCHPO
23	90.5	4.8	344	1	ULB6_HCMVA
24	88.5	4.8	376	1	P086_FUGRU
25	88	4.7	1037	1	VH1V_ECOLI
26	86.5	4.6	430	1	CINA_MYCTU
27	86	4.6	636	1	YNR6_YEAST
28	86	4.6	503	1	PODX_MOUSE
29	85.5	4.6	376	1	MID2_YEAST
30	85	4.6	583	1	CH12_CANAL
31	85	4.6	812	1	FGRI_XENLA
32	85	4.6	812	1	FGRI_XENLA
33	85	4.6	1718	1	RRPO_SHVX

34	84.5	4.5	440	1	T10B_HUMAN
35	84.5	4.5	678	1	VLD3_AGRRH
36	84.5	4.5	1049	1	TR45_HUMAN
37	84.5	4.5	1058	1	UR41_HUMAN
38	84.5	4.5	2738	1	PCGV_RAT
39	84.5	4.5	5376	1	ZAN_MOUSE
40	84	4.5	536	1	CNA_MOUSE
41	84	4.5	1640	1	CH42_HUMAN
42	83.5	4.5	586	1	EC4H_ECOLI
43	83.5	4.5	655	1	CD4_MOUSE
44	83.5	4.5	881	1	YDH8_YEAST
45	83.5	4.5	903	1	ECIC_BOVIN

ALIGNMENTS

RESULT 1
VGLI_VZVD
ID VGLI_VZVD STANDARD; PRT; 354 AA.
AC P09258;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycoprotein I precursor (Glycoprotein IV) (GI) (GPV).
GN 67
OS Varicella-zoster virus (strain Dumas) (VZV).
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Alphaherpesvirinae; Varicelloviruses.
CC NCBI_TaxID=10338;
OK [1]
RN SEQUENCE FROM N.A. PubMed=3018124;
RP MEDLINE=86306557;
RA Davidson A.O., Scott J.E.
RT The complete DNA sequence of varicella-zoster virus.
RL J. Gen. Virol. 67:1759-1816(1986).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=84131932; PubMed=6321154;
RA Davidson A.O.;
RT "DNA sequence of the US component of the varicella-zoster virus genome."
RL EMBO J. 2:2203-2209(1983).
[3]
RN MOTAGENESIS, AND PHOSPHORYLATION SITE.
RP MEDLINE=94267879; PubMed=8207795;
RA Yao Z., Grose C.;
RT "Unusual phosphorylation sequence in the gpIV (gI) component of the varicella-zoster virus gpI-gpIV glycoprotein complex (VZV gE-gI complex)."
RL J. Virol. 68:4204-4211(1994).
[4]
RN -1 SUBUNIT: HETERODIMER OF GPV AND GPI (GE).
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 SIMILARITY: TO HERPESVIRUSES GLYCOPROTEINS I, AND TO PRV GP63.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

EMBL: X04370: CAA27950.1; -
EMBL: X00208: CAA25032.1; -
PIR: F27345: VGH67;
DR InterPro: IPR002874: Herpes_gI.
DR Pfam: PF01688: Herpes_gI.1.
KW Glycoprotein; Phosphorylation; Transmembrane; Signal.
FT SIGNAL 1 354
FT CHAIN 18 295 GLYCOPROTEIN I.
FT DOMAIN 18 295 POTENTIAL.
FT TRANSMEM 296 312 POTENTIAL.

[illegible]

```

CC or send an email to license@lsb-slb.ch).
DR EMBL, L07067, AAA47888.1; -.
DR PIR, C46113, C46113.
DR InterPro: IPR002874; Herpes_g1.
DR Pfam: PF01688; Herpes_g1.1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 353 GLYCOPROTEIN 1.
FT DOMAIN 21 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 293 POTENTIAL.
FT DOMAIN 294 353 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 40 40 POTENTIAL.
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 353 AA; 40470 MW; E0314F7B5B0E84A2 CRC64;

Query Match 8.3%; Score 155; DB 1; Length 353;
Best Local Similarity 20.2%; Pred. No. 1.le-05;
Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11.

QY 18 EG---AMGIVTGNHVSARIDDD--HIYIVADREPATQLOLFEPMGQRP-HKPYSGIVR 71
   || || || || || || || || || || || || || || || || || || || || ||
DB 20 FGIQCAALIIYGRNYISLVNSSATSIFLKGNNNDASIGRFLFGDQFPVNTYNTVAVE 79
   || || || || || || || || || || || || || || || || || || || || ||

QY 72 VAFRSDINOCQOELESEEFENCTHRSSSVFYGCKV-TEYTESASNRILGPHPKRLTR 130
   || || || || || || || || || || || || || || || || || || || || ||
DB 80 L-LHVNOTTLCLQPIRYRVYGECPPIRTGAILACRKKSMHENTQILDPEVEITFFKN 138
   || || || || || || || || || || || || || || || || || || || || ||

QY 131 NRPNDSCMFYIVVFLDDTKEPIDVFAIOLSVYQFANTATRGLYSKASCRTFGLEPTVOL 190
   || || || || || || || || || || || || || || || || || || || || ||
DB 139 NTKVEDAGIYLLVQLDIT-SLFDLFEFVSLANYPRQDINSMEVNT-----EPYVS 188
   || || || || || || || || || || || || || || || || || || || || ||

QY 191 EAY-LRTEESWRNQOAYVATEATTSSAEATPTPTPVATASASELEADHFTPEMLENGVDHY 249
   || || || || || || || || || || || || || || || || || || || || ||
DB 189 PSHLNTFKIKCHKFPVHNGMEQSIQHIYVT-----SDVDETENLSMQKDLGST 238
   || || || || || || || || || || || || || || || || || || || || ||

QY 250 EPTPANENSNVTVRL-----GTMSPTLIGTVAAVYASATIGLVIVISI-TRNNC 298
   || || || || || || || || || || || || || || || || || || || || ||
DB 239 QKPRKNENPDKAVVNTHTHTRKTLMESSADVFEMIAVPTASLSLVITAIIVTVGIYRRRS 298
   || || || || || || || || || || || || || || || || || || || || ||

QY 299 TPWRKLDIVSQDDERSQTRRE 320
   || || || || || || || || || || || || || || || || || || || || ||
DB 299 SEKKRIYRPKRTEQASTEKRE 320
   || || || || || || || || || || || || || || || || || || || || ||

RESULT 3
VGLI_HSVGB STANDARD; PRT; 424 AA.
AC P18553:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein 1 precursor.
GN GN OR 73.
OS Equine herpesvirus type 1 (strain Abdp) (EHV-1),
OS Equine herpesvirus type 1 (strain ABI) (EHV-1), and
OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OS Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31520, 10328, 10330;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-ABdp;
RC MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
FL Virology 189:304-316(1992).
[2]

```


RP SEQUENCE FROM N.A.
RP STRAIN-ABI:
RC MEDLINE-91276272; PubMed-1647359;
RX Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
RA Boness W.A.:
RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
RT herpesvirus type-1 short unique region.",
RL Gene 101:203-208(1991).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN-Kentucky D:
RX MEDLINE-91108393; PubMed-2177089;
RX Audonnet J.-C., Winslow J., Allen G., Paolletti E.:
RT "Equine herpesvirus type 1 unique short fragment encodes
RT glycoproteins with homology to herpes simplex virus type 1 gD, gI and
RT gE".
RT J. gen. Virol. 71:2969-2978(1990).
CC -1- SURCELLULAR LOCATION: Type I membrane protein.
CC -1- SUBUNIT: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPV,
CC -1- SUBUNIT: TO OTHER HERPESVIRUSES GLYCOPROTEINS I.

This SWIS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announcements> or send an email to license@isb-sib.ch).

--
CC EMBL; M86664; AAB02508.1; -
DR EMBL; M36299; AAA66547.1; -
DR PIR; C36645; VGBPE9.
DR PIR; J00998; J00998.
DR PIR; A36803; VGBB34.
DR InterPro; IPRO02874; Herpes_gI.
DR Pfam; PF01688; Herpes_gI_1
KW Glycoprotein; Signal; Transmembrane.
FT SIGNAL 21 422 POTENTIAL.
FT FT 23 316 GLYCOPROTEIN I.
FT DOKLIN 33 316 EXTRACELLULAR (POTENTIAL).
FT TRANSHEM 320 340 POTENTIAL.
FT DONALIN 341 424 CYTOPLASMIC (POTENTIAL).
FT FT 35 35 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAG...) (POTENTIAL).
FT FT 78 78 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAG...) (POTENTIAL).
SEQUENCE 424 AA; 46392 MW; EE9BEF7DA895806 CRC64;

Query Match	8.2%	Score 153.5%	DB 1	Length 424
Best Local Similarity	23.8%	Pred. No. 1.9e-09		
Matches	Conservative 70	Mismatches 41	Indels 57	Gaps 12
QY	1	MASTLGLALLAATLAPGANGIYITGNVHASRIDDDIYVAPREARITOL-QLEFMPG	59	
DB	1	MAKLTFGSAILLISMAICSAIYIYREHMSMYLVASSEFVYPTDSSLVLGHLFLFDG	60	
QY	60	QR-QHKKYSGTVAVAFRSDITNOCYOLSEEFENCTRRSSSVVGC-KVETFFSASN	116	
DB	61	ORLPTMYSGLIEL-IHNVSYCVYIQTISYESCPVYANNAARSLKHTSKHNDYER	119	
QY	117	RLTPEPPEFLITRNPRDSCGMFYVVRLLDTKEPIYFVALIOLSVYOFANNTAATGLYS	176	
DB	120	VNASEVENYVLNATIKPOPTDSCAVILVKKLDHA-PLAVYFVSASFYDL-----	167	
QY	177	KASCRITGLPTVQ---LEAALIRTEESMRMCAQYVATEATTS---AEATTPRYVATNSA	229	
DB	168	KSKIVPDPMPETIOTVEPTTYSVYSTPYTDYDVTTESTSTSTQOAMNSTOP-SAWWG	226	
QY	230	SELEAEHFTTPEMLENGVDVHYEPTPEANNSVTVRLG-----TWSPLT	271	

Db 227 TQLTTE-----LPTNE---TWIGQFALCHWFQPSRVPTL 260

RESULT 4	AC	ID	VLGI_PRIVRI	STANDARD:	PRT:	350 AA.
	P07646;					
DT	01-APR-1988					
DT	01-APR-1988					
DT	15-JUL-1999					
DE	Glycoprotein Gp63 precursor.					
OS	Pseudorabies virus (strain R1a) (PRV).					
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;					
CC	Alphaherpesvirinae; Varicelloviruses.					
CC	NCBI_TaxId=10350;					
RP	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=86308235; PubMed=3018284;					
RA	Petrovskis E.A., Timmins J.G., Post L.E.;					
RP	"Use of lambda gtl1 to isolate genes for two pseudorabies virus					
RP	glycoproteins with homology to herpes simplex virus and varicella-					
RP	zoster virus glycoproteins";					
RL	J. Virol. 60:185-193(1986).					
CC	1. SUBCELLULAR LOCATION: Type I membrane protein.					
CC	1. SIMILARITY: TO OTHER HERPESVIRUS GLYCOPROTEINS I, AND TO VZV					
CC	GPVI.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	the European Bioinformatics Institute. There are no restrictions on its					
CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/).					
CC	or send an email to license@isb-sib.ch).					

DR	EMBL: M4336; AAC35204.1; -.			
DR	PIR: A29012; VGBB63.			
DR	InterPro: IPR002874; Herpes_g1.			
DR	Pfam: PF01688; Herpes_g1; 1.			
KM	Glycoprotein; Transmembrane;			
ET	SIGNAL	1	23	Signal.
ET	CHAIN	24	350	OR 27 (POTENTIAL).
ET	DOMAIN	24	285	GLYCOPROTEIN GP63.
ET	TRANSMEM	308	308	EXTRACELLULAR (POTENTIAL).
ET	DOMAIN	309	350	POTENTIAL.
ET	CARBOHYD	56	56	CYTOPLASMIC (POTENTIAL).
ET	CARBOHYD	73	73	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	CARBOHYD	256	256	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	CARBOHYD	262	262	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	CARBOHYD	275	275	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	350 AA:	36773 MW:	66A22A95EC21BDEA.CRC64;

	Query Match	Score 143.5;	DB 1;	Length 350;
	Best Local Similarity	72.8%;	Pred. No. 0.0001;	
Matches	82;	Conservative	42;	Mismatches 149; Indels 87; Gaps 17

Qy	8	LALLAATLAPFGAM--GIYITGNVARSIDDDIIVUAPREATTIOLETFMPCORPKP	65
		: : : : : : : : : :	
Dd	15	LILAALITALPRPGGVLPFGAGSVNVAAGSLVLPGDAANLTIDETLFLFEGHSPSN-	73
Oy	66	YSGVVARAFPSDITINOCYOELSEEFNCNHRSSVFQC--KTXYEFSAS-----NR_L	118
		: : : : : : : : : :	
Dd	74	YSGRVEL-LYDKKRCSTREVAAEDULCPRVNHAEFRCLRKREPARRASAALVEARLL	132
Oy	119	TGRPHRKLTIIRNPDSNGMFUYILVDYDTKPIDVGLTOLSYUOPANTAFRLG----	174
		: : : : : : : : : :	
Dd	133	-----LVSRPARPDAGSVLVLRVNVT---TDLFVLTAUV-----PRKHGRHP	174
Oy	175	--SKASCRTFGILPYOLEAVILTEESRMMAQMU--ATEATTS-----AAETTPPV	224
		: : : : : : : : : :	
Dd	175	TPSSADECR---PVV-----GSMDLSLVADPRADAFTPTTRPEEPPTTPARP	221

QY 225 TATSAS-----ELEHEFTFWLGVNDHYEPTPANSNTVRLGTMSPLTIGTVA 277
 DB 222 RGATGATPEPRSDDEEED-----EGATTAAMPVPCTGLDANGM---VLTASVSVRL 271
 QY 278 AVVSATIG-----LVIVISIVTRNCTPHRLDLYSODDEERSQTRRSRK 323
 DB 272 AAANAATGANGPGKIAMVLPCTIVLILFVGVAACARCARCAGTASTGRDPAARSTR 331
 RESULT 5
 VGLI_HSVBS STANDARD; PRT; 380 AA.
 ID VGLI_HSVBS
 AC 008102;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glycoprotein I.
 GN GI.
 OS Bovine herpesvirus type 1.2 (strain ST).
 OC Alphaherpesvirinae; Varicelloviridae;
 NCBI_TaxID=45407;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94167875; PubMed=8122370;
 RA Leung-Trick P., Audonnet J.F., Riviere M.;
 RT "The complete DNA sequence and the genetic organization of the short
 RT unique region (US) of the bovine herpesvirus type 1 (ST strain).";
 RL Virology 199;409-421(1994).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GRIV,
 CC AND TO PRV GP63.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: 223068; CA80605.1;
 CC DR InterPro: IPR002874; Herpes_gI.
 CC DR Pfam: PF01688; Herpes_gI.
 CC KW Glycoprotein.
 FT CARBOHYD 67
 FT SEQUENCE 380 AA; 39910 MW; AEBELFB9BA30D2BD CRC64;
 SQ
 Query Match 7.5%; Score 140.5; DB 1; Length 380;
 Best Local Similarity 25.3%; Pred. No. 0.0002;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
 QY 1 MASLLGLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATIQL--QLFFMP 58
 DB 1 MRCLLLMNVYLAARAP--ARSLVYGEAVGLADGPVAAVAP--TDATLALGRLIFLE 57
 QY 59 GQAP-HKPSGIVRAFRSITNOCEOESEEPENCNTHRSSVFGCKVETTESASNR 117
 DB 58 HQPAGRRNGVEL-LRYHAAGDCFVMLOTTAFASCPRVANNAFSCILADRRPARSER 116
 QY 118 LTGP--PHPEKLTIRNRPDMSGMFYIVRL---DDTKPEIVVPAIQLSVYQFA----- 166
 DB 117 RASAVENHVLVSIAIRPRPDSGLYFLRVGITYGTAGSEKRRRVFFLAFAVHSFGEGDP 176
 QY 167 -----NTAATRGILYKASCRFTGL-----PTVQLEAVYRTESWR 201
 DB 177 EAAARTPARSRQSRPASGLTSSASLYDALANSPOAPPRPARPAARAGRRPRRYDE 236
 QY 202 NMOAVATEVTTTSACATPTPTTATSAS 230
 DB 237 TTEVAATRASAFALTTPAGPTASPA 265
 RESULT 6

CD4_MOUSE
 ID CD4_MOUSE STANDARD; PRT; 457 AA.
 AC P06332;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
 DE T4/Leu-3) (T-cell differentiation antigen L3T4).
 GN CD4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87018845; PubMed=3094146;
 RA Tourville B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;
 RT "Isolation and sequence of L3T4 complementary DNA clones: expression
 RT in T cells and brain.";
 RL Science 234:610-614(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87115821; PubMed=3027575;
 RA Littman D.R., Gettner S.N.;
 RT "Unusual intron in the immunoglobulin domain of the newly isolated
 RT murine CD4 (L3T4) gene.";
 RL Nature 325:453-455(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=88152875; PubMed=3326818;
 RA Parnes J.R., Hunkapiller T.;
 RT "L3T4 and the immunoglobulin gene superfamily: new relationships
 RT between the immune system and the nervous system.";
 RL Immunol. Rev. 100:109-127(1987).
 RN [4]
 RP SEQUENCE FROM N.A. (BRAIN FORM).
 RC TISSUE=Brain;
 RX MEDLINE=88041159; PubMed=283269;
 RA Gorman S.D., Tourville B., Parnes J.R.;
 RT "Structure of the mouse gene encoding CD4 and an unusual transcript
 RT in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98112780; PubMed=9445485;
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RT "Comparative sequence analysis of a gene-rich cluster at human
 RT chromosome 12p13 and its syntenic region in mouse chromosome 6.";
 RL Genome Res. 8:29-40(1998).
 RN [6]
 RP SEQUENCE OF 27-43.
 RX MEDLINE=86166694; PubMed=3082751;
 RA Claesson B.J., Tsagaratos J., Kirsbaum L., Maddox J., McKay C.R.,
 RA Brandon M., McKenzie I.F.C., Walker I.D.;
 RT "The L3T4 antigen in mouse and the sheep equivalent are
 RT immunoglobulin-like.";
 RL Immunogenetics 23:129-132(1986).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=86233454; PubMed=3086886;
 RA Claesson B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
 RT "Partial primary structure of the T4 antigens of mouse and sheep:
 RT assignment of intrachain disulfide bonds.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4493-4503(1986).
 CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
 CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
 CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

```

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M36850: AAA39401.1; -
DR EMBL: M3816: AAA37267.1; -
DR EMBL: X04836: CAA28539.1; -
DR EMBL: M36851: AAA39402.1; -
DR EMBL: M17080: AAA37403.1; -
DR EMBL: M17078: AAA37403.1; JOINED.
DR EMBL: AC002397: AAC36010.1; -
DR PIR: A02110: NMST4
DR PIR: A26038: A26038.
DR HSP: P01730: IMR.
DR MGD: MGI:88335; CD4.
DR InterPro: IPR000973: CD4_TcRg.
DR InterPro: IPR003006: Ig_MHC.
DR InterPro: IPR003600: Ig_Like.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR PRINTS: PR00692: CD4TCANTIGEN.
DR SMART: SM00410: IG_Like; 2.
DR SMART: SM00406: IGV; 1.
KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW Immune response; Repeat; Signal; Lipoprotein; Palmitate;
KW Alternative splicing.
FT SIGNAL 1 26
FT CHAIN 27 457 T-CELL SURFACE GLYCOPROTEIN CD4.
FT DOMAIN 27 394 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 395 417 POTENTIAL.
FT DOMAIN 418 457 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 128 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 129 207 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 208 317 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 318 374 IG-LIKE C2-TYPE DOMAIN 3.
FT CARBOHYD 187 187 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT DISULFID 42 112
FT DISULFID 159 158
FT DISULFID 328 370
FT LIPID 418 421 PALMITATE (BY SIMILARITY).
FT LIPID 421 421 PALMITATE (IN BRAIN-SPECIFIC ISOFORM).
FT VARSPLIC 1 240 MISSING (IN BRAIN-SPECIFIC ISOFORM).
SQ SEQUENCE 457 AA; 51296 MW; 1B1DA7527CB00F33 CRC64.

Query Match 6.2%; Score 115; DB 1; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.035;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

OY 19 GAMGIVITGNHVSARIDDDHIVAPREATTIOLDF--FMDGPRHPRVSGTVRAFR 75
DB 93 GSPLIT--NKLKMDQSOTVCELENKRE--EVELMVKYFSGTSLLOGSTLTLLDSN 149
OY 76 SDITNOCVOELSEERFENCGRSSVFCVKYTEXTSASNRLTGPHPFKLTINRPN 135
DB 150 SKVSN---PLTE-----CKHKKGVSSGSKV-----LSMNLMLVQ 181
OY 136 DSGMEFVYRIIDDDKREPDVFAIOLSVYOFANTATRGVSKASCRTGLPVLQEAFLR 195
DB 182 DSDFMNCYITLDQK---NMFGMTLSVLGFSTAIT--AYKSEGSSEFSPINFAE--- 233
OY 196 TERSARN--WQAYVATEFTTTSAAETTPPVATASASLEAHEHTFPLMENGVDHYEPTP 253
DB 234 -ENGKGLMKKA-----EKDSFQFWISFSIKKREYSV 265

OY 254 ANENSNVTVLGTMSPTLIGTVAAVVSATIGVIVISITRNCTPRKLDVYSDDEE 313
DB 266 QKSTKDLKLTKEPILTLTKIPVSLQFASGNL---TLTLDKCTLHGEVNLVKKVAQ 321
OY 314 RSQRRRSRRKFGPMVACEIN-----KGADD---SELVELVAIVNPSA----- 353
DB 322 LNNI-----LICEVAGPTSPKMLTLKQENQEARVSEOKVGVVAPETGMQCL 371
OY 354 LSSPDSIKM 362
DB 372 LSEGDVKYM 380

RESULT 7
ID VGL1_HSV11 STANDARD; PRT; 390 AA.
AC P06487;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycoprotein 1.
GN GI OR US7.
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP MEDLINE=8516822; PubMed=2984429;
RX McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
RT "Sequence determination and genetic content of the short unique
RT region in the genome of herpes simplex virus type 1."
RL J. Mol. Biol. 181:1-13(1985).
JC 1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
JC 2: GH, GB, GC, GG, GD, GI, AND GE.
JC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS 1, TO VZV GP1V,
JC AND TO PRV GP63.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: L00036: AAA96681.1; -
DR EMBL: X14112: CAA32284.1; -
DR EMBL: X02138: CAA26061.1; -
DR PIR: A05243: OOB877.
DR InterPro: IPR002874: Herpes_g1.
DR Pfam: PF01688: Herpes_g1; 1.
KW Glycoprotein.
FT CARBOHYD 156 156 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 390 AA; 41369 MW; 39381B1D65F08C8 CRC64.

Query Match 6.1%; Score 113.5; DB 1; Length 390;
Best Local Similarity 20.8%; Pred. No. 0.038;
Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;

OY 7 TIALIANTAPFGAMGIVITGNHVSARIDDDHIVAPREATTIOLDFMFGORHPR 65
DB 27 TVSLVSNSEVDAGALG-----PDGVVEEDLLITG-----ELRFVGDDVPPHY 69
OY 66 YSGYRVAFSDITNOCVOELSEERFENCGRSSVFCVKYTEXTFASNRLTGPHP 125
DB 70 YDGVVEL-WHYPKQHCPRVIVVVTACPRPVAALCRATDSYHS-----PAYPP 121
OY 126 -----KLTINRPNDSGMFVYRIIDDDKREPDVFAIOLSVYOGFANTATRLQYS 176

```



```

OS Herpes simplex virus (type 2 / strain 333).
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae: Simplexvirus.
OC NCBI_TaxID=10313;
RX MEDLINE=86291145; PubMed=3016980;
RA Hodgman T.C., Mason A.C.;
RT The herpes simplex virus type 2 equivalent of the herpes simplex
RT virus type 1 US7 gene and its flanking sequences."
RL Virology 153:1-11(1986).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M14886; AAA45861.1;
DR EMBL: D00026; BA00021.1;
DR PIR: A05246; Q08E88;
DR InterPro: IPR002874; Herpes_g1.
DR Pfam: PF01688; Herpes_g1; 1.
KW Glycoprotein.
FT CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA; 39548 MW; B83A9E2D20D8AD3D CRC64;

Query Match 5.78; Score 107; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.12;
Matches 74; Conservative 51; Mismatches 163; Indels 64; Gaps 13;

OY 3 SLGCTALLAATLAPGAMGIVITGNHVSARIDDDHIVAPREPTIOL-----OLFF 56
DB 5 SLOG-LAIIGLWMC--ATGLVVRGPTVSL-VSDSLVDAGAVGPGFVEDLAVFGELEHF 59
OY 57 MPOGRPKPYSGTVRAFRSDITNOCYOELSERFENCYHRSSESVFVGCVKVETYSASN 116
DB 60 VQAQVPHNTNYDDIIELFHYPLGNHCPRVVHVVTLTACRRPAVAFTLCRSTHANS--- 116
OY 117 RLTGPPIHF-----KLITRNPRNDGMEFYIVRLDD-TKEPIDVFAIQLSYVQFA 166
DB 117 ----PAYPTLEGLARQPLRLVTRATRDYAGLYLVWVGSATNLSFLGLVALS---A 168
OY 167 NTAATRGLYSKASCTFGILPTVOLEAVLRTESRMWQAVVATEATTSAEATTPPVTA 226
DB 169 NGTFVYNGSDYGCDAQPL-----FSAPRLGPSVYTPGASRPPTPT 212
OY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSVYRLCTMSPTLIGTVAAVVSATIGL 286
DB 213 TTPSSPRDPTPAPG----DGTGTPAPASGRIAPPNSTSASESHRLTLVAQVOLAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRRESKRGF-MVACEINKKA 336
DB 268 STIAFVELGSCICFIHRC-----QRRRRRPGQIYNPGVGCANVEAA 310

RESULT 10
VGLI_HSV2H STANDARD; PRT; 372 AA.
ID VGLI_HSV2H
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glycoprotein I.

```

```

GN GI OR US7.
OS Herpes simplex virus (type 2 / strain HGS2).
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae: Simplexvirus.
OC NCBI_TaxID=10315;
RX MEDLINE=87111457; PubMed=3027242;
RA McGeoch D.J., Moss H.W.M., McNab D., Frame M.C.;
RT "A sequence and genetic content of the HindIII 1 region in the
RT short unique component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons".
RL J. Gen. Virol. 68:19-38(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87111457; PubMed=3027242;
RA McGeoch D.J., Moss H.W.M., McNab D., Frame M.C.;
RT "A sequence and genetic content of the HindIII 1 region in the
RT short unique component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons".
RL J. Gen. Virol. 68:19-38(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X04798; CA28485.1;
DR EMBL: 286099; CAB06714.1;
DR PIR: F43674; F43674.
DR InterPro: IPR002874; Herpes_g1.
DR Pfam: PF01688; Herpes_g1; 1.
KW Glycoprotein.
FT CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA; 39558 MW; C0D4A22CAB16E8D7 CRC64;

Query Match 5.38; Score 99; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.58;
Matches 74; Conservative 49; Mismatches 165; Indels 64; Gaps 13;

OY 3 SLGCTALLAATLAPGAMGIVITGNHVSARIDDDHIVAPREPTIOL-----OLFF 56
DB 5 SLOG-LAIIGLWMC--ATGLVVRGPTVSL-VSDSLVDAGAVGPGFVEDLAVFGELEHF 59
OY 57 MPOGRPKPYSGTVRAFRSDITNOCYOELSERFENCYHRSSESVFVGCVKVETYSASN 116
DB 60 VQAQVPHNTNYDDIIELFHYPLGNHCPRVVHVVTLTACRRPAVAFTLCRSTHANS--- 116
OY 117 RLTGPPIHF-----KLITRNPRNDGMEFYIVRLDD-TKEPIDVFAIQLSYVQFA 166
DB 117 ----PAYPTLEGLARQPLRLVTRATRDYAGLYLVWVGSATNLSFLGLVALS---A 168
OY 167 NTAATRGLYSKASCTFGILPTVOLEAVLRTESRMWQAVVATEATTSAEATTPPVTA 226
DB 169 NGTFVYNGSDYGCDAQPL-----FSAPRLGPSVYTPGASRPPTPT 212
OY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSVYRLCTMSPTLIGTVAAVVSATIGL 286
DB 213 TTPSSPRDPTPAPG----DGTGTPAPASGRIAPPNSTSASESHRLTLVAQVOLAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRRESKRGF-MVACEINKKA 336
DB 268 STIAFVELGSCICFIHRC-----QRRRRRPGQIYNPGVGCANVEAA 310

RESULT 11

```

```

P200. MYCPN      STANDARD:      PRT: 1036 AA.
AC      P75211: 050346;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Protein P200.
GN      P200 OR MPN567 OR MP275.
OS      Mycoplasma pneumoniae.
OC      Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX      NCBI_Taxid=2104;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 29342 / M129;
RX      MEDLINE=96257197; PubMed=8675035;
RA      Proft T., Hilbert H., Plagens H., Herrmann R.;
RT      "The P200 protein of Mycoplasma pneumoniae shows common features with
RT      the cytochrome-associated proteins HMW1 and HMW3."
RN      Gene 171:79-82(1996).
RN      (2)
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 29342 / M129;
RX      MEDLINE=97105885; PubMed=8948633;
RA      Himmelfreisch R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RT      Herrmann R.;
RT      "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT      pneumoniae."
RN      Nucleic Acids Res. 24:4420-4449(1996).
RN      (3)
RP      SEQUENCE OF 641-678 FROM N.A.
RC      STRAIN=ATCC 29342 / M129;
RX      MEDLINE=95075318; PubMed=7984111;
RA      Proft T., Herrmann R.;
RT      "Identification and characterization of hitherto unknown Mycoplasma
RT      pneumoniae proteins."
RN      Mol. Microbiol. 13:337-348(1994).
CC      -1- FUNCTION: PROTEIN CYTOSKELETON-ASSOCIATED WHICH COULD BE AN
CC      ACCESSORY STRUCTURAL COMPONENT IN CYTOCHERANCE.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC      The European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC      or send an email to license@isb-sdb.ch).
CC      -----
DR      EMBL: U25989; AAC9815.1;
DR      EMBL: AE000027; AAB95923.1;
DR      EMBL: Z32646; CAA83569.1;
CC      Cytochrome; Structural protein; Repeat; Complete proteome.
FT      DOMAIN 277 280 POLY-THR.
FT      DOMAIN 300 845 PRO-RICH.
FT      DOMAIN 357 360 POLY-THR.
FT      DOMAIN 401 404 POLY-ALA.
FT      DOMAIN 718 781 3 X 6 AA REPEAT OF E-P-E-P-N-F.
FT      REPEAT 718 723 1.
FT      REPEAT 738 743 2.
FT      REPEAT 776 781 3.
FT      REPEAT 776 781 3.
FT      CONFICT 641 641 A -> P (IN REF. 3).
SQ      SEQUENCE 1036 AA: 116915 MW; DESAEBAAB6DD95B29 CRG64;

  Query Match      5.3%; Score 99; DB 1; Length 1036;
Best Local Similarity 23.9%; Pred. No. 2.2;
Matches 57; Conservative 29; Mismatches 90; Indels 62; Gaps 10.

Oy      127 LTRRRPRDSCMFVYIRLDDTKRPIDVFAIQLSVYQFAN---TAATRGLSKASCRFF 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy      446 VVINDGQFOQAGFHFVVVDLST-APLTVAELELOEOELVNEFVTTTSRETTTFASTPVF 504
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      184 G---LPTVQLEAYLTETESWMRMQAVVATETATTSAAETTP---TPVATGSASELAEVH 236
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      505 EPPVAPITVESEQLLENE---G-----FVESIVVATSNRPVASTPVET----- 546
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

OY 237 FTFPMLENGVDEHPTPANENSNTVRLGTMSPTLLIGV-----AAVVSATITL 286
DB 547 -----VELTE-TPVSLSEPLEVVOLETAAYVETVYVTKAAYEPVLAAYEAPLAV 596
OY 287 VIVISIVTRNMCTTPRRKLDVTSQDDEERSQTRRESRKFG--PMVACEINKGADODSEL 342
DB 597 EPIVETST-----TLAAETVEEAQVQESNAVAVEPALETESKATSEAOAEL 643

RESULT 12
ID YD76_MYCPN STANDARD: PRT; 1140 AA.
AC P75405;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN376 (A19_0rfl140).
GN MPN376 OR MP460.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN375.
CC -1- SIMILARITY: IN THE CENTRAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN374.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN373.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000045; AAB96108.1; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 1098 1118 POTENTIAL.
SQ SEQUENCE 1140 AA; 130383 MW; 8FA9406C57D8886 CRC64;

Query Match 5.3%; Score 98.5; DB 1; Length 1140;
Best Local Similarity 20.5%; Pred. No. 2.7; Indels 91; Gaps 15;
Matches 68; Conservative 53; Mismatches 119;

OY 71 RVAFAFSDDITNOC-YOELSEERFE-NCTHRSSVFQCKVTEYTFASASNRLTGPHPFKLT 128
DB 660 RERFKDINNIYKXGCISETETIKVAHVKVDMLMARSDPKLAS---VOSTAKKYGLN 736
OY 129 IIR-NRPNDSCGFYIV-----RLDDTK-----EPIDVFAIQLSVYOPAN-- 167
DB 737 LRSNRY---TGQFYVVVVVTNANDIGNORANNAKSYFYIEGLDKGAOSSYLVRFEENQ 793
OY 168 -----TAATRGYKSKASCTPCLPLVYQLEAYLRTES-----WRMGOVYVATEATT 213
DB 794 KLYSLESIAVDSDRGILYK-----NVSKAIIQAQONOLYLDTHNMWNA--ALKAWL 842
OY 214 TSAEATPTPTPVATSGASELEAHEFTFPMLENGVDHDEPTPANENSNTVRLGTMSPTLLG 273
DB 843 TNAELTILPT-ASADNSAKLS-----TPNAENE-----GFLEENYSG 878
OY 274 VTVAAVASATIGLVIVISIVTRNM-----CTPHRKLDVTSQDDEERSQTRRE 320

```


CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: 272974; CAA97215.1; -
 DR EMBL: X99074; CAA67525.1; -
 DR HSSP: P23904; IAKR.
 DR SGD: S0003421; CRH1.
 DR InterPro: IPR000757; Glyco_hydro_16.
 DR Pfam: PF00722; Glyco_hydro_16; 1.
 KM Hypothetical protein.
 FT DOMAIN 63 66 POLY-SER.
 FT DOMAIN 301 310 POLY-SER.
 FT DOMAIN 345 357 POLY-SER.
 FT DOMAIN 387 391 POLY-SER.
 FT DOMAIN 467 470 POLY-SER.
 SO SEQUENCE 507 AA; 52757 MW; 7D7B61F57AE942C CRC64;

Query Match 5.3%; Score 98; DB 1; Length 507;
 Best Local Similarity 21.7%; Pred. No. 1.1;
 Matches 54; Conservative 46; Mismatches 95; Indels 54; Gaps 9;

136 DSCMFVYVRLDPTKEPIDVFAIQLSVQFAPNTAATRGVSKASCTFFGLPTVQLEAYLR 195
 278 DGGSTI--GRYDQAEQDFAVLANGSISSTSVSSASTSVSSVSSSTSSASST 335
 196 TEESNRMOAVYATETTTSAETPTPTVATSELEAEHETFPMLNCGVDHYEPTPAN 255
 336 VSSS---VSTVSSSSSVSSSSSTSPSSSTATSKTLASSVT---TSSSISFE-KOSS 388
 256 ENSNVTVRLCTMSPTLIGT-VAAYVSATIGLVIVISYTRNCTPHKRLDTVSD- 310
 389 SSSKKTVAASSTSESISSSKTPATVSS-TRSTVAAPTQOSSVSSDSPVO 438
 311 -----DEESQTRRESKRFPMV-----ACEIKKGADQ-----S 340
 439 DRGCVATSSNDVTSSTTQISKTTSTIQSSSEASSTNSVOISNGADLAOSLPREGKLP 498
 341 ELVELVAIV 349
 499 VLVALLALL 507

RESULT 15
 ID SLN1_YEAST STANDARD: PRT; 1220 AA.
 SLN1_YEAST
 AC P39928;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 OS Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
 GN SLN1 OR YIP2 OR YIL147C.
 ON Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / YPH1;
 RC STRAIN-S288C / YPH1;
 RX MEDLINE-94024010; PubMed-8211183;
 RA Ota I.M., Varshavsky A.;
 RT "A yeast protein similar to bacterial two-component regulators,"
 RL Science 262:566-569(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RC STRAIN-S288C / AB972;
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Lewis S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
 RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Ralsh S.V., Whitehead S.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE-94239498; PubMed-8183345;
 RA Maeda T., Wurgler-Murphy S.M., Saito H.;
 RT "A two-component system that regulates an osmosensing Map kinase
 RT cascade in yeast,"
 RL Nature 369:242-245(1994).
 CC -1- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
 CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SKR2/SSK2->
 CC PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
 CC PROTEIN TO ACTIVATE SKR2 AND SSK2, TWO MARKERS THAT FURTHER
 CC STIMULATE THE PBS2-HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
 CC THE ACTIVATED SLN1 HISTIDINE KINASE REPRESENTS THE ACTIVATION OF THE
 CC PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
 CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: 238059; CAA86131.1; -
 CC EMBL: 001835; AAC48912.1; -
 CC PIR: S48888; S48888.
 CC PIR: S48387; S48387.
 CC HSSP: P06143; IUDR.
 DR SGD: S0001409; SLN1.
 DR InterPro: IPR003594; AtPbind_AtPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR003661; His_Kina.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; response_reg; 1.
 DR Pfam: PF00512; signal; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR ProDom: PD000039; Response_reg; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HSKA; 1.
 DR SMART: SM00448; REC; 1.
 DR PROSITE: PS50109; HIS_KIN; 1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
 DR Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane.
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT DOMAIN 47 333
 FT TRANSMEM 334 354
 FT DOMAIN 355 1220
 FT DOMAIN 573 928
 FT DOMAIN 1089 1210
 FT MOD_RES 576 576
 FT MOD_RES 1144 1144
 FT CARBOHYD 100 100
 FT CARBOHYD 138 138
 FT CARBOHYD 142 142
 FT CARBOHYD 181 181
 FT CARBOHYD 224 224
 FT CARBOHYD 272 272
 FT MUTAGEN 576 576
 FT MUTAGEN 891 891
 FT MUTAGEN 1144 1144
 SO SEQUENCE 1220 AA; 134434 MW; 45FEE24A8165486B CRC64;

Tue May 6 18:37:35 2003

us-09-993-777-68.rsp

Page 11

Query Match	5.28;	Score 97;	DB 1;	Length 1220;
Best Local Similarity	32.78;	Prod No 4;		

Best Local Similarity 22.7%; Pred. NO. 4;
Matches 58; Conservative 43; Mismatches 104; Indels 50; Gaps 11.

QY 5 LGTLALATLAPFGAMGIVITGNHVSARIDDDHIVIVAPREATTIQLQLFFMPGQRPKH 64

db 32 LGSLLIAVT-----TGVYFTSNYKNLR--SDRLYIAQLKSSQIDQTLNYL----YYQ 79

65 PYSGTVRAFRSDITNOCYQELSEERFENCTH-----RSSVFCVCTEYTF---SA 114

Db 80 AYLASRDALQSSLTSYAGNKSADNWDLSYIQKFLSSNLPYAKVYDSSFNAVLNA 139

115 SNRLTGPHP-----FKLTIRNPRNDSCMFYIVRLDTKEPIDVEAIQLSVYQFAN 167

Db 140 T NNGCTGDLIPEDVLDLFLPLSTDPPLP--SSLETIGILTDPVLNSTD-YLMSMSLP IFAN 1966

168 TAATRGLYSKASCRPTGLPIVQLAAYLRTEESWRNQAYVAITEATTTSAEATTPPTVAT 227

```

197 PSII---LTDSPVGYITIMSA-----EGLKSVFNDTALHSTIAISAV 240

```

228 SASELEAE--HTTP 240

Db 241 YNSQGKASGYHFEVP 255

```

.
search completed: May 3, 2003, 10:13:39
job time : 17.5 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:08:23 ; Search time 28 seconds

(without alignments)
2663.895 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863

Sequence: 1 MASLIGTLLAATLAPFGA.....VELVAIVNPSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :
1: SP_ARCHAEA:
2: SP_BACTERIA:
3: SP_FUNGI:
4: SP_HUMAN:
5: SP_INVERTEBRATE:
6: SP_MAMMAL:
7: SP_MHC:
8: SP_ORGANELLE:
9: SP_PLANT:
10: SP_PROTOZOA:
11: SP_VIRUS:
12: SP_VIRUS:
13: SP_VIRUS:
14: SP_VIRUS:
15: SP_VIRUS:
16: SP_VIRUS:
17: SP_VIRUS:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	12	067645 gallid herp
2	164	8.8	420	12	039309 equine herp
3	162.5	8.7	354	12	098VNI human herp
4	158	8.5	420	12	055525 equine herp
5	156	8.4	384	12	069357 feline herp
6	154	8.3	384	12	066931 feline herp
7	152	8.2	355	12	096615 turkey herp
8	149	8.0	355	12	069287 turkey herp
9	148	7.9	364	12	09YPA1 canine herp
10	147	7.9	364	12	041525 canine herp
11	147	7.9	359	12	091335 canine herp
12	145	7.8	370	12	096789 phocid herp
13	140.5	7.5	369	12	091E39 bovine herp
14	139.5	7.5	382	12	039505 pseudorabid
15	130.5	7.0	366	12	099F67 turkey herp
16	125	6.7	356	12	088524 turkey herp

17	124.5	6.7	683	12	036401	036401 alicetaphine
18	123	6.6	355	12	067638	067638 gallid herp
19	115	6.2	433	11	055054	055054 mus musculu
20	115	6.2	457	11	061396	061396 mus musculu
21	108.5	5.8	319	5	09W357	09W357 drosophila
22	106.5	5.7	235	12	09DY19	09DY19 bovine herp
23	103	5.5	982	5	09VIG1	09VIG1 drosophila
24	102.5	5.5	378	4	09W415	09W415 homo sapien
25	102.5	5.5	4498	5	09W223	09W223 drosophila
26	99	5.3	279	5	09U474	09U474 caenorhabdi
27	97.5	5.3	1011	5	09NH29	09NH29 helleoverpa
28	97.5	5.2	1714	5	09W1X4	09W1X4 drosophila
29	96.5	5.2	814	13	091897	091897 xenopus lae
30	96	5.2	877	4	09H306	09H306 homo sapien
31	96	5.2	878	4	09H307	09H307 homo sapien
32	96	5.2	957	4	014651	014651 homo sapien
33	96	5.2	1217	4	09UKW9	09UKW9 homo sapien
34	95.5	5.1	332	12	08V0L9	08V0L9 equine herp
35	95.5	5.1	337	12	08V0M1	08V0M1 equine herp
36	95.5	5.1	342	12	08V0L8	08V0L8 equine herp
37	95.5	5.1	356	12	08V0L7	08V0L7 equine herp
38	95.5	5.1	357	12	08V0M2	08V0M2 equine herp
39	95.5	5.1	372	12	08V0M3	08V0M3 equine herp
40	95.5	5.1	374	12	08V0L6	08V0L6 equine herp
41	95.5	5.1	389	12	08V0M0	08V0M0 equine herp
42	95.5	5.1	826	12	08V0L5	08V0L5 equine herp
43	95.5	5.1	867	12	039782	039782 equine herp
44	95	5.1	745	5	09VJ38	09VJ38 drosophila
45	95	5.1	1844	5	022579	022579 caenorhabdi

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	362 AA.
ID	067645		
AC	067645		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	Glycoprotein I.		
OS	Gallid herpesvirus 1.		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.		
OX	NCBI_TaxID=10386;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-USDA CHALLENGE STRAIN:		
RX	MEDLINE=9703380; PubMed=8879127;		
RA	Wild M.A., Cook S., Cochran M.;		
RT	"A genomic map of infectious laryngotracheitis virus and the sequence		
RT	and organization of genes present in the unique short and flanking		
RT	regions."		
RL	Virus Genes 12:107-116(1996).		
DR	EMBL; U28832; AAC5101.1; -		
DR	InterPro: IPR002874; Herpes_g1.		
DR	Pfam: PF01688; Herpes_g1; 1.		
SO	SEQUENCE 362 AA; 39750 MW; F530C1A7CC6BA5 CRC64;		
Query Match	100.0%; Score 1863; DB 12; Length 362;		
Best Local Similarity	100.0%; Pred. NO. 1.3e-160;		
Matches 362; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MASLIGTLLAATLAPFGANGIVITGNHVSARIDDDHIVIAAPPETIQLQFFMPGQ 60		
DB	1 MASLIGTLLAATLAPFGANGIVITGNHVSARIDDDHIVIAAPPETIQLQFFMPGQ 60		
QY	61 RPHKPYGAVRAFRSDITNOCYOELESEERENCTRRSSVVGCKVTEYFSSNRLTG 120		
DB	61 RPHKPYGAVRAFRSDITNOCYOELESEERENCTRRSSVVGCKVTEYFSSNRLTG 120		
QY	121 PPHFKLTITRNPRDNGMFYIVRLDQTEPIDVAIQLSVYGFANAAATRGITSNASC 180		

```
Db 121 PPHFEKLTINRPNDGMYIVRLDDTKEPDIQVFAIQLSVQFANTATRGYSKASC 180
Qy 181 RTFCLPTVQLEAVYLRTEESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 240
Db 181 RTFCLPTVQLEAVYLRTEESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 240
Qy 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVISIVTRNCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVISIVTRNCTP 300
Qy 301 HRKLDVTSQDEERSQTRRESRKGPVACEINKGADQDSEVELVAIVNPSALSSPDSI 360
Db 301 HRKLDVTSQDEERSQTRRESRKGPVACEINKGADQDSEVELVAIVNPSALSSPDSI 360
Qy 361 KM 362
Db 361 KM 362

RESULT 2
039309 PRELIMINARY; PRT; 420 AA.
AC 039309:
DT 01-JUN-1998 (Tremblrel. 05, Created)
DT 01-JUN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Counterpart of HSV-1 gene US7 and VZV gene 67.
GN 73.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
ON NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed=9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4."
RL J. Gen. Virol. 79:1197-1203(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RX Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030027; AAC59593.1;
DR InterPro: IPR002874; Herpes_g1.
DR Pfam: PF01688; Herpes_g1.1.
SQ SEQUENCE 420 AA; 45710 MW; 1EB944825DF3D852 CRC64;

Query Match 8.8%; Score 164; DB 12; Length 420;
Best Local Similarity 25.5%; Pred. No. 1.8e-06;
Matches 96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;

Db 10 LLAATLAPFGAMGIVTGNHVSARIDDDHVIYAPREAIQL-QLEFMGQR-PHPRYS 67
Qy 13 LLAISMCK---ATAITYGEHSMYLNASSSEFAYPKDKSLVVGCHMLDTGQRLPTTNS 69
Db 68 GTVAFAFRSDITNOCYOELSEERFENCTHRSSSVFVCC--KTEYTSASNRLLTGPHP 125
Qy 70 GLEEL-IHHYNSRCYCVITQITISGCPRYANNAFRSCLIKTSHNDYTHVNTSVETNV 128
Db 126 KLTIRNRPNDGMYIVRLDDTKEPDIQVFAIQLSVYOF-ANTAAATRGISKASCTFG 184
Qy 129 LLNITRPOPADSGAYILRVKLHNA-PTADVFGSAFYLDQSNTPVPEPPTAKEPSNVFT 187
Db 185 LPTVQLEAVYLRTEESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 241
Qy 188 RTPAPAPANTSTK-----TGSNTTSSOSTWLTLPPTP-----RPA 221
Qy 242 LKNGVDHYEPTPANEN--SNVTYRL-----GTMSPT-----LIGVTAAVVSATIG-- 285
Db 222 LEL---HLTTPANETVYSGDTAMLCGFRPSTAVPTIYHMLGLT-----GNLPE 269
```

```
Qy 286 --LVIVISIVTRNCTP-HRKLDVTS-----QDEERSQTRRESR-KRGPVY----ACEIN 333
Db 270 DVLIEDSEILR---FPPRPQQTSSRTEDGDKQTSTSPKSRNKIYAVNVIPTACVLM 326
Qy 334 KGADQDSEVELVAIVN 350
Db 327 -----LLLVVGAIIIN 337

RESULT 3
098VN1 PRELIMINARY; PRT; 354 AA.
AC 098VN1:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE ORF67.
OS Human herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
ON NCBI_TaxID=10335;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RX MEDLINE=21109116; PubMed=11162813;
RA Faga B., Maury W., Bruckner D.A., Grose C.;
RT "Identification and Mapping of Single Nucleotide Polymorphisms in the Varicella-zoster Virus Genome."
RL Virology 280:1-6(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RA Cole N.L., Faga B.P., Grose C.;
RX Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-VIA;
RA Grose C., Faga B.;
RT "Identification and mapping of single nucleotide polymorphisms in the varicella-zoster virus genome."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF314221; AAK19249.1;
DR EMBL: AF325441; AAK01055.1;
DR InterPro: IPR002874; Herpes_g1.
DR Pfam: PF01688; Herpes_g1.1.
SQ SEQUENCE 354 AA; 39373 MW; 3F01739F3AFC6B08 CRC64;

Query Match 8.7%; Score 162.5; DB 12; Length 354;
Best Local Similarity 22.4%; Pred. No. 2e-06;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

Qy 23 IVTGNHVSARIDDDHVIYAPRE--ATIQLEFMGQR-HRYSQTVAFRRSDI-78
Db 21 LTRKGDHVSQVASSLSLTIIPQNDNYTEIKQVLFISQLTGTGNTSSTLELLY-ADT 79
Qy 79 TNOCYOELSEERFENCTHRSSSVFVCCYV--EYTFASNRLLTGPHPKLTIRNRP 135
Db 80 VACPFNSVQIVRYDCPRIRTSAFISCRYKSHWYGNSTDRISTEPDAGVMLKTRPGIN 139
Qy 136 DSGMFYIVRLDDTKEPDIQVFAIQLSVY-----QANPAATAGLYSKAS 179
Db 140 DAGVVYVLLVRLDHSRS-TDGFILGVNVYTAGSHNINIGVLYTSPSLONGYSTRALFOQA- 197
Qy 180 CRTFGGLPT-----VQLEAVYLRTEES-WRNMQAYVATATTSAEATPTPT 225
Db 198 -RLCDLPATPKGSGTSLFQHMLDRAGKSLIEDPMLH-EDVYTTETKSVYKKG----- 248
Qy 226 ATSASELEHFTFPWLENGVDHYEPTPAN--ENS-----NVTYRLGTMSPTLIGVTV 276
Db 249 -----IEN---HYVPTDMSTLPEKSLNDPEPMLL-----IIPYA 281
Qy 277 AAVVSATIGLVISIVTRNM 297
```


ID	OC9PAL		PRELIMINARY;	PRT:	364 AA.
DT	01-MAY-1999	(TReMBLrel. 10,	Created)		
DT	01-JAN-1998	(TReMBLrel. 10,	Last sequence update)		
DT	01-JUN-2001	(TReMBLrel. 17,	Last annotation update)		
DE	Similar to HSV-1 gi.				
OS	Canine herpesvirus.				
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Alphaherpesvirinae.				
OX	NCBI_Taxid=37110;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CSL-2;				
RC	MEDLINE=98185505; PubMed=9524817;				
DR	Tyack S.G., Studdert M.J., Johnson M.A.;				
DR	Nucleotide sequence of canine herpesvirus homologues of herpes simplex virus type 1 US2, US3, glycoproteins I and E, US6.5 and US9 genes.";				
RL	DNA Seq.: 7,365-368(1997).				
DR	EMBL: U49380; AAC67213.1. -				
DR	Interpro: IPRO02874; Herpes_gI.				
DR	Interpro: IPRO01304; Lectin.C.				
DR	Ffam: PF01688; Herpes_gI: 1.				
SMARI	SMART: SM00034; CLECT: 1.				
SO	SEQUENCE 364 AA; 41999 MW; B9HC33EE/FB913A9 CRC64;				
Query Match		7.9%; Score 148; DB 12: Length 364;			
Best Local Similarity	27.3%, Pred No 4, 2e-05;				
Matches	45; Conservative 30; Mismatches 82; Indels 8; Gaps				
OY	4	LCTGALLAAATAPAGAMGYTGTVGNHYASARIDDDHIVAVRPRPATLOLFDPNGGR-P 62			
DB	16	LITMLPLPLEFLXGVGFYYKTYISMTFNSSGSFIPDCKFIYSGRLLFDLDHLHS 75			
OY	63	HKPSCGVAVARSQITNOCCOELSEERFENCTHRSSVFGC--KVTEYTSASRLTG 120			
DB	76	VNNNSGTIERI---HNNSCYTVQTVEFYECSPRFNFNASFCCLKVKSHNESOLIRINS 132			
OY	121	PPHPFKLTTRNPDSGMFVIYLRDDTPREPIDFAQLSYVOF 165			
DB	133	IENGVLLEITNRKPDMSGVFYLRVOLENNK--TDVGIGPARYSF 175			
SULT 10					
JD	041525	PRELIMINARY;	PRT:	364 AA.	
AC	041525;				
DT	01-JAN-1998	(TReMBLrel. 05, Created)			
DT	01-JAN-1998	(TReMBLrel. 05, Last sequence update)			
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)			
DE	CUG7 (Glycoprotein 1).				
GN	G.I.				
OS	Canine herpesvirus.				
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Alphaherpesvirinae.				
OX	NCBI_Taxid=37110;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Haanes E.J., Tomlinson C.;				
RM	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-YPI1M0;				
RC	MEDLINE=98455388; PubMed=9784067;				
RA	Nishikawa Y., Xuan X., Otsuka H.;				
RT	"Identification and characterization of the glycoprotein E and I genes of canine herpesvirus.";				
RN	Virus Res. 56:77-92(1998).				
RN	[3]				

```

SEQUENCE FROM N.A.
STRAIN-AUSTRALIAN:
Reudel G.H., Pekin J., Webb-Magn K., Hardy C.M., D, G, H and I, thymidine
"Nucleotide sequence of glycoprotein genes B, D, G, H and I of an
rt kinase and protein kinase genes and gene homologue UL 24 of an
Australian isolate of canine herpesvirus."
Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: U84223; AAB67059.1; -
DR EMBL: AB003729; BAA33765.1; -
DR EMBL: AF361076; AAK51063.1; -
DR InterPro: IPR002874; Herpes_g1.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF01688; Herpes_g1; 1.
DR SMART: SM00034; Clecty; 1.
SQ SEQUENCE 364 AA; 42068 MW; 08BC32EF7B913A8 CRC64;

Query Match
Best Local Similarity 7.9%; Score 148; DB 12; Length 364;
Matches 45; Conservative 50; Mismatches 82; Indels 8; Gaps 4;

4 LIGTALLAATLAPGAMGIVITGNHVASRIDDHIVYAPREATTILOLFFMPGCR-P 62
16 LITTMPLILFELTGNGEYVYKGTIYSMLNTSSGFSIFPDCKTIFYSGRLFLNDQHL 75
63 HKPYSCTVAVAFSDITNOCYOELESEEPENCSTRSSVYGC--KTEYTFSSNRNLG 120
76 VNNSCTIETI---HFNNSCTIVYOTIETESCPRIFFNNAFSLCKVSKHHSQLRINS 132
121 PPHPEKLTINRPNDSCGFVYVIRLDDTKPRIDVFAQLSLVYOF 165
133 IENGVLLETINPKRNDSCGFVFINQLENNK--TDVFIPAFIYSF 175

RESULT 11
ID 091335 PRELIMINARY; PRT: 259 AA.
AC 091335:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein I.
OS Canine herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae.
OX NCBI_Taxid=37110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DED-6;
RX MEDLINE=98455388; PubMed=9784067;
RT Nishikawa Y., Xuan X., Otsuka H.;
RT "Identification and characterization of the glycoprotein E and I genes
of canine herpesvirus."
RL Virus Res. 56:77-92(1998).
DR EMBL: AB003728; BAA33764.1; -
DR InterPro: IPR002874; Herpes_g1.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF01688; Herpes_g1; 1.
DR SMART: SM00034; Clecty; 1.
SQ SEQUENCE 259 AA; 29965 MW; 66C7A9A957FF7ED0F CRC64;

Query Match
Best Local Similarity 7.9%; Score 147; DB 12; Length 259;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

4 LIGTALLAATLAPGAMGIVITGNHVASRIDDHIVYAPREATTILOLFFMPGCR-P 62
16 LITTMPLILFELTGNGEYVYKGTIYSMLNTSSGFSIFPDCKTIFYSGRLFLNDQHL 75
63 HKPYSCTVAVAFSDITNOCYOELESEEPENCSTRSSVYGC--KTEYTFSSNRNLG 120
76 VNNSCTIETI---HFNNSCTIVYOTIETESCPRIFFNNAFSLCKVSKHHSQLRINS 132
121 PPHPEKLTINRPNDSCGFVYVIRLDDTKPRIDVFAQLSLVYOF 165
133 IENGVLLETINPKRNDSCGFVFINQLENNK--TDVFIPAFIYSF 175

```

```

DB 133 IENGVLLEITNRPNDGIVFTRVLENNK--TDVFGIDAFITSF 175
RESULT 12
ID 086789 PRELIMINARY: PRT: 370 AA.
AC 086789;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein gI.
OS Feline herpesvirus (Feld herpesvirus 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94267406; PubMed=8207390;
RA Spatz S.J., Rota P.A., Maes R.K.;
"Identification of the feline herpesvirus type 1 (FHV-1) genes
encoding glycoproteins G, D, I and E: expression of FHV-1 glycoprotein
D in vacinia and raccoon poxviruses."
RL J. Gen. Virol. 75:1235-1244(1994).
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI.
SQ SEQUENCE 370 AA; 41568 MW; 2A816ECB37466A77 CRC64;

Query Match
Best Local Similarity 7.8%; Score 145; DB 12; Length 370;
Matches 72; Conservative 52; Mismatches 136; Indels 66; Gaps 14;

QY 5 LCTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPRE-ATIQQLFFMPGQ-RP 62
DB 1 MSIAFIYILMAIGYVYRGDHLVDSSGFVITPLENTIYGHLEFLDQRP 60
QY 63 HRPSTGVAVARSDITNOCYOLSEERENCTHSSSVFVGC--KVTEYTSASRLTG 120
DB 61 VNNYNGTLEI-IHYNHSSCYKIVQIEYSSCPVRNNAFRSCLHKTSMHQDLSINTS 119
QY 121 PPHPKLITRNPRNDGMEFYIVRLDTPKEPIDVFAIOLSVQFANTATGLYSKASC 180
DB 120 VETGMLITTSRKMEDGILALVRPNHNK-ADVFGLSVFYSF---DTRGHRHHADE 174
QY 181 RTFG--LPTVQ-LEAVLRTESRMNQAY---VATEATTSAEATTPPTVATSASELA 234
DB 175 NUNGEILTPSPMEYVKV----NTPYDHWTTGTSTNKSMSSEPSNTSISC----- 223
QY 235 EHFPTFWLENGDHYEPTANENSNTVRL-----GIMSPLIGTVAA 278
DB 224 -----HTFQNDPNEGELTYLHLINAGNITYDDVMQGTTLKPRLI----- 264
QY 279 VVSATIGLIVISIVTRNCTPHRLDT 306
DB 265 ----DMGLNLSTSSFKN--GNHAKKDT 286

RESULT 13
QY 091E39 PRELIMINARY: PRT: 369 AA.
ID 091E39;
AC 091E39;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Glycoprotein I.
OS Phocid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=47418;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN-PB84;
RA Martina B., Osterhaus A.D.M.E., Harder T.C.;
RT "Identification and analysis of immunogenicity of the glycoprotein D
RT equivalent within the unique short segment of phocid herpesvirus-1."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ290955; CAC51466.1;
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI.
SQ SEQUENCE 369 AA; 42372 MW; 1587181704A7A8A CRC64;

Query Match
Best Local Similarity 7.5%; Score 140.5; DB 12; Length 369;
Matches 57; Conservative 36; Mismatches 89; Indels 45; Gaps 10;

QY 22 GIVITGNHVSARIDDDHIYVAPRE-EATIQQLFFMPGQ-RP-PHKYSGTVRVAFRSDIT 79
DB 16 GIVYRGTYMSMYNTSSGTVYRDDDFVNTGYLLFLDQRLPVTYSGTIEIT--FN 72
QY 80 NCOYOLSEERENCTHSSSVFVGC--KVTEYTSASA---SNRLTGPHPKLITRNPR 133
DB 73 YCYTYVQTEYVSCPRINNAFRSCLIKYSKHQSQLRINSIEFG---VLEIKNPK 128
QY 134 PNDGMEFYIVRLDTPKEPIDVFAIOLSVQFANTATGLYSKASCRTFGLPTVQLEAV 193
DB 129 PSDSGVYITRVQLENNK--TDVFGISAIFYSEKSG--ENIRKPDSDN----- 173
QY 194 LRTEESRMNQAYVATEATTSASA-----TTPPTVATSASEL 232
DB 174 -----ENFTNHLVTPSTTISRKPRESETSHLNTFPTDIPAPYCHEV 213

RESULT 14
QY 039505 PRELIMINARY: PRT: 382 AA.
ID 039505;
AC 039505;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein I.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JURA;
RA Goltz M., Buhk H.J., Brohl H., Lewin M., Mankertz A., Boernar B.,
RA Borchers K., Weigelt W.; to the EMBL/Genbank/DBJ databases.
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 372-382 FROM N.A.
RC STRAIN-JURA;
RA Schwyzer M.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JURA;
RA Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vlcek C.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-COOPER;
RA Goltz M., Buhk H.J., Schwyzer M.;
RT "Nucleotide sequence of the HindIII O and K fragments located in the
RT US region of the bovine herpesvirus 1 genome."
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ004801; CAA06146.1;
DR EMBL: Z98199; CAB10890.1;
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI.
SQ SEQUENCE 382 AA; 39596 MW; 0F06C95CD2581EC2 CRC64;

```


Query Match	7.58;	Score 139.5;	DB 12;	Length 382;
Best Local Similarity	24.78;	Pred. No. 0.00027;		
Matches 67; Conservative	37;	Mismatches 122;	Indels 45;	Gaps 10;

[illegible]

RESULT 15	ID	099F67	PRELIMINARY;	PRT:	366 AA.
AC	099F67				
DT	01-JUN-2001	(TEMBLrel, 17, Created)			
DT	01-JUN-2001	(TEMBLrel, 17, Last sequence update)			
DT	01-DEC-2001	(TEMBLrel, 19, Last annotation update)			
DE	Glycoprotein 1.				
GN	GI.				
OS	Pseudorabies virus.				
OC	Viruses; dsDNA viruses, no RNA stage: Herpesviridae;				
OC	Alphaherpesvirinae; Varicellovirus.				
OX	NCBI_TaxID=10345;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=EA;				
RC	Xiao S.B., Chen H.C., Fang L.R., Wang G.F., Ma X.R., Hong W.Z.;				
RT	"Cloning and sequence analysis of the gi gene of Pseudorabies virus Ba				
RT	and expression in insect cells. "				
RL	and Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				
RR	EMBL: AF306511; AAG53092.1; -;				
RR	InterPro: IPR002874; Herpes_gi				
DR	InterPro: IPR002965; P_rtlh_extensn.				
DR	Pfam: PF01688; Herpes_gi, 1.				
DR	PRINTS: PRO1217; PRICHEX15N.				
DR	SEQUENCE 366 AA; 38609 MW; 862696A4712BAF20 CRC64;				

Query Match	7.08;	Score 130.5;	DB 12;	Length 366;
Best Local Similarity	24.78;	Pred. No. 0.0016;		
Matches	76;	Conservative	30;	Mismatches 129;
			Indels	73;
			Gaps	16

QY 8 LALLAAATLAPPGAM--GIYITGNHVSARIDDDHIVVAPREATITOLELFPMGQRPKPF 65
 15 LLLAALLTALLAPRGVGLFRCAGVSVHAGSAVLAPGDANLITDGTLLLEFGSPSN- 73
 QY 66 YGCVYRAVAPSDITNOCYOGLSEEPFNCYTHRSSYFVGC--KTYETFTSAS----NRL 114
 74 YGSRNEL-LALDRKACTYRETAAYEDLCRYNHEHFRGCLRKPEPLARASAAVYARLL 133
 QY 119 TCRPRFKLLTINRPNRDSGMVYIVYLLDQTEPRIDYRILQSLSYQOANTATRLYSKA 178
 133 -----LEFSRPSAGSDMGISVYKVRNNGT--TDLEFTRALV-----PPRGPPVPT 174
 QY 179 S-----CRFGGLPTVOLLEAYLQTEBSNRN-----MOAYVATATTSAAETPPVPT 225
 Db 175 SEPDADECK-----PVV-----GSHMDSLRYVDPADEAVFTQPPREPERPTAPPR 221

Oy 226 ATSA-----SELAE---HFFPPLANGVDHYEPFPAENSNVTVRLGMSPTLLGVYA 277
| | | | : | : | : | :
Db 222 GGCATPEPRDDEEBEDATTTPTL-----TPAPGLDANGTM---VLNSVSVRLL 271

Oy 278 AVYASNTIG 285
| : || |
Db 272 AAANATNG 279

```
Search completed: May 5, 2003, 16:14:39
Job time : 29 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Comphen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:14:43 ; Search time 16.5 Seconds
(Without alignments)
1893.078 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1663

Sequence: 1 MASLIGTALATLAPFGA.....VELVALVNSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/p/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/p/ptodata/2/pubpaa/PCR_NEW_PUB.pep.*
- 3: /cgn2_6/p/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/p/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/p/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/p/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/p/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep.*
- 8: /cgn2_6/p/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/p/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/p/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/p/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/p/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/p/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/p/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1863	100.0	362	10 US-09-881-457A-5	Sequence 5, Appl 1
2	148	7.9	364	9 US-10-156-275-56	Sequence 56, Appl 1
3	115	6.2	612	9 US-10-125-692-10	Sequence 10, Appl 1
4	112	6.0	387	9 US-10-114-893-133	Sequence 133, Appl 1
5	108	5.8	713	10 US-09-801-368-408	Sequence 408, Appl 1
6	102.5	5.5	379	9 US-09-813-153-138	Sequence 138, Appl 1
7	97	5.2	1220	10 US-09-801-368-332	Sequence 332, Appl 1
8	93	5.0	320	9 US-09-738-626-5621	Sequence 5621, Appl 1
9	92.5	5.0	547	10 US-09-753-436-1	Sequence 1, Appl 1
10	91	4.9	365	9 US-09-870-759-73	Sequence 73, Appl 1
11	90.5	4.9	359	9 US-09-978-295A-45	Sequence 45, Appl 1
12	90.5	4.9	359	9 US-09-978-697-45	Sequence 45, Appl 1
13	90.5	4.9	359	9 US-09-978-192A-45	Sequence 45, Appl 1
14	90.5	4.9	359	9 US-09-999-832A-45	Sequence 45, Appl 1
15	90.5	4.9	359	9 US-09-978-189-45	Sequence 45, Appl 1
16	90.5	4.9	359	9 US-10-174-590-42	Sequence 42, Appl 1
17	90.5	4.9	359	9 US-10-176-758-42	Sequence 42, Appl 1
18	90.5	4.9	359	9 US-10-175-737-42	Sequence 42, Appl 1
19	90.5	4.9	359	9 US-10-173-706-42	Sequence 42, Appl 1

20	90.5	4.9	359	9 US-10-175-738-42	Sequence 42, Appl 1
21	90.5	4.9	359	9 US-10-175-752-42	Sequence 42, Appl 1
22	90.5	4.9	359	9 US-10-176-482-42	Sequence 42, Appl 1
23	90.5	4.9	359	9 US-10-176-757-42	Sequence 42, Appl 1
24	90.5	4.9	359	9 US-10-176-913-42	Sequence 42, Appl 1
25	90.5	4.9	359	9 US-10-180-552-42	Sequence 42, Appl 1
26	90.5	4.9	359	9 US-10-180-557-42	Sequence 42, Appl 1
27	90.5	4.9	359	9 US-10-173-700-42	Sequence 42, Appl 1
28	90.5	4.9	359	9 US-10-174-572-42	Sequence 42, Appl 1
29	90.5	4.9	359	9 US-10-174-579-42	Sequence 42, Appl 1
30	90.5	4.9	359	9 US-10-174-582-42	Sequence 42, Appl 1
31	90.5	4.9	359	9 US-10-174-588-42	Sequence 42, Appl 1
32	90.5	4.9	359	9 US-10-175-739-42	Sequence 42, Appl 1
33	90.5	4.9	359	9 US-10-175-740-42	Sequence 42, Appl 1
34	90.5	4.9	359	9 US-10-175-743-42	Sequence 42, Appl 1
35	90.5	4.9	359	9 US-10-176-488-42	Sequence 42, Appl 1
36	90.5	4.9	359	9 US-10-176-492-42	Sequence 42, Appl 1
37	90.5	4.9	359	9 US-10-176-747-42	Sequence 42, Appl 1
38	90.5	4.9	359	9 US-10-176-750-42	Sequence 42, Appl 1
39	90.5	4.9	359	9 US-10-176-985-42	Sequence 42, Appl 1
40	90.5	4.9	359	9 US-10-176-987-42	Sequence 42, Appl 1
41	90.5	4.9	359	9 US-10-176-991-42	Sequence 42, Appl 1
42	90.5	4.9	359	9 US-10-176-992-42	Sequence 42, Appl 1
43	90.5	4.9	359	9 US-10-176-993-42	Sequence 42, Appl 1
44	90.5	4.9	359	9 US-10-184-658-42	Sequence 42, Appl 1
45	90.5	4.9	359	9 US-10-173-695-42	Sequence 42, Appl 1

ALIGNMENTS

```
RESULT 1
US-09-881-457A-5
Sequence 5, Application US/09881457A
Patent No. US20020081316A1
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Cook, Stephanie M
TITLE OF INVENTION: No. US20020081316A1 Avian Herpes Virus and Uses Thereof
FILE REFERENCE: SY010510KOK
CURRENT APPLICATION NUMBER: US/09/881,457A
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/426,352
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/804,372
PRIOR FILING DATE: 1997-02-21
PRIOR APPLICATION NUMBER: PCT/US95/10245
PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: 08/663,566
PRIOR FILING DATE: 1996-06-13
PRIOR APPLICATION NUMBER: 08/288,065
PRIOR FILING DATE: 1994-08-09
PRIOR APPLICATION NUMBER: PCT/US93/05681
PRIOR FILING DATE: 1993-06-14
PRIOR APPLICATION NUMBER: 08/023,610
PRIOR FILING DATE: 1993-02-26
PRIOR APPLICATION NUMBER: 07/898,087
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 362
TYPE: PRT
ORGANISM: Infectious Laryngotracheitis Virus
US-09-881-457A-5
Query Match 100.0% Score 1863; DB 10; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.5e-16; Indels 0; Gaps 0;
Matches 362; Conservative 0; Mismatches 0;
|||||MASLIGTALATLAPFGAMGIVTGNHNSARIDDDHIYVAPPEATLOLOLFEMPG 60
|||||
```

Db 1 MASLCTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPAITQLOLFPMQ 60
Qy 61 RPKPYSCTVRAVFRSDITNOCYQLSEERFENCSTRSSSVFGCKVTEYTFASNRLTG 120
Db 61 RPKPYSCTVRAVFRSDITNOCYQLSEERFENCSTRSSSVFGCKVTEYTFASNRLTG 120
Qy 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASC 180
Db 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASC 180
Qy 181 RTGGLTVOLEAVLRTESRNQAVATATTSATPTPVATTSASELAEHPTTP 240
Db 181 RTGGLTVOLEAVLRTESRNQAVATATTSATPTPVATTSASELAEHPTTP 240
Qy 241 WLENGVDHEPPRPNANSVTYRLGTMSPPLIGTVAAVVSATIGLVIVISYTRNKCPT 300
Db 241 WLENGVDHEPPRPNANSVTYRLGTMSPPLIGTVAAVVSATIGLVIVISYTRNKCPT 300
Qy 301 HRKLDVVSODDERSTRRSRKFGPMVACEIKKGADDOSELVLAIVNPSALSSPDSI 360
Db 301 HRKLDVVSODDERSTRRSRKFGPMVACEIKKGADDOSELVLAIVNPSALSSPDSI 360
Qy 361 KM 362
Db 361 KM 362

RESULT 2
US-10-156-275-56

Sequence 56, Application US/10156275
Publication No. US20030049844A1

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.

Frank, Rexann S.

TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES

NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/156,275

FILING DATE: 28-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/399,118

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/680,726

FILING DATE: 12-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-46-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-10-156-275-56

Query Match 7.9%; Score 148; DB 9; Length 364;
Best Local Similarity 27.3%; Pred. No. 16-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
Qy 4 LGCTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPAITQLOLFPMQ 62
Db 16 LITMFLPLIFLFLYGVNGVYKGYTISMFLNLSGFSIFPDDKFTVSGSLDLDQHS 75
Qy 63 HKPYSCTVRAVFRSDITNOCYQLSEERFENCSTRSSSVFGCKVTEYTFASNRLTG 120
Db 76 VNNYSCTIERI--HNNSCYTYQTIEYFSCRINNMFRSLKRVSKHNEQLINNS 132
Qy 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQF 165
Db 133 IENGVLLEITNPKRNDSGYFIRVQLENNK--TDVEGIDAFIVSF 175

RESULT 3
US-10-125-692-10

Sequence 10, Application US/10125692
Publication No. US2003004429A1

GENERAL INFORMATION:

APPLICANT: Aderem, Alan

APPLICANT: Hayashi, Fumitaka

APPLICANT: Smith, Kelly D.

APPLICANT: Underhill, David M.

APPLICANT: Ozinsky, Adrian

TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods

FILE REFERENCE: P-15 5155

CURRENT APPLICATION NUMBER: US/10/125,692

CURRENT FILING DATE: 2002-04-17

PRIOR APPLICATION NUMBER: US 60/285,477

PRIOR FILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 612

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-692-10

Query Match 6.2%; Score 115; DB 9; Length 612;
Best Local Similarity 20.6%; Pred. No. 0.026;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

Qy 19 GAMGIVITGNHVSARIDDDHIVAPREPAITQLOLF--FMPGPRPKPYSGTVRAFR 75
Db 93 GSPLIIT--NKLKMDSSQYICLENKRE--EVLNWFKTYFSGTSLDQOSLTLTLDN 149
Qy 76 SDITNOCYQLSEERFENCSTRSSSVFGCKVTEYTFASNRLTGPPHPKLTIRNPPN 135
Db 150 SKVSN---PLTE---CKHKKGKVVSGSKV-----LSMSNLRVQ 181
Qy 136 DSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASCRTFGIPYQLEAYLR 195
Db 182 DSDFMNCTVTLQDK--NMFGMTLSVLGQSAIT--AVKSDEESAEEFPLNFAF---- 233
Qy 196 TEESMRN--WQAVVATEATTSAETTPPVATTSASELAEHPTTPLENGVDHEPTP 253
Db 234 -ENGNGELMKKA-----EKDSFPPWISFSIKNNEVY 265
Qy 254 ANSNSVTYRLGTMSPPLIGTVAAVVSATIGLVIVISYTRNMCPTPHRKIDTVSODDE 313
Db 266 OKSTKDLKQLKRETLPLTLKIPVSLQFAGSGL---TLTDKGLHDEVNLVAKVAAQ 321
Qy 314 RSQTRRESRKFGPMVACEIN-----KGADD--SELVELVAINPSA----- 353
Db 322 LNNT-----LNCVEVWGTPSPMRRLTLAQENQEARVSEQKYVAVAPETGLMOCL 371
Qy 354 LSEPSIRK 362
Db 372 LSEGDVKM 380

RESULT 4
US-10-114-893-133
Sequence 133, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, David
APPLICANT: Merberg, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKenough
APPLICANT: Kelleher, Kerry S.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 133
LENGTH: 387
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-893-133

Query Match 6.0% Score 112; DB 9; Length 387;
Best Local Similarity 19.2% Pred. No. 0.026;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

DB 1 MASLGLTALATLAPGAGIYITGNHNSARIDDDHYIYAPPEPTLOLQTFMPCQ 60
12 USCLAGVSVQYTI-PDGFVAVVGSNVLLICI-YTTVASRQSLQSMF----- 62
QY 61 RPKKPSGTVAVAFRSDITNOCYQELSEEFENCIRSSSVYVCGKTYEYFASNRITG 120
DB 63 --HKKEPISITF-----SOGQAVAG-----QPKRITIG 92
QY 121 PPHF--FKLTIRNPNDGMYIYVRLDTKEPDIYFAIOLSVYQFANTATGSLSKA 178
93 SNDGNASTITSHMOPADSGY----ICDVNNPPPLDQONOGILANSVLYKP-----SKT 143
QY 179 SCRTFGLP---TVOLEAVLRTEESWRNMOAYVATEATTSATPTPTPTATISASLEA 234
DB 144 LCSYQGRPETGHTISLSCL-----SALGTPSPV----- 171
QY 235 EHFTFPMLENGVDHYEPTPANENSNVY-----RLG----- 265
DB 172 ----YVM--HKLEGRDIVVKKENFPTTGLIVIGNLTNEQGYOCTAINRLGNSCEID 225
QY 266 -TMSPTLIGVYAAVVSATIGLVIVISIVTFNNMCTPHRKLDIVSODDEERSQTRRESKRF 324
DB 226 LTSSHPEVIGIIVGALIGSVGAIIISYV----CFANRKKAKAK--ERNSKTTAE--L 276
QY 325 GPVAVCEINKGADODS---ELVELVAIYNPSAL--SSPDSIK 361
DB 277 EFWT--KINPRGESEAMPREDATOLEVTLPPSIHETGPDTIQ 316

RESULT 5
US-09-801-368-408
Sequence 408, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian

APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofia
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 408
LENGTH: 713
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-408

Query Match 5.8% Score 108; DB 10; Length 713;
Best Local Similarity 27.3% Pred. No. 0.15; 89; Indels 46; Gaps 11;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

DB 60 QRPKPSGTVAVAFRSDITNOCYQELSEEFENCIRSSSVYVCGKTYEYFASNRITG 115
DB 86 QRHQILASLTVQQRQ000000VQ000000QLAASASVPVADQPPATISATATPAA 144
QY 116 NRTGPPHPKLTIRNPNDGMYIYVRLDTKEP-----D 154
DB 145 NTTGSISAE--PVQASRPNLVGS-----OLPTTLVVSNAQQLPQ00LQ00LQ00 197
QY 155 VFAIQLSVYQFANTATRGLYSKASCRTFGLPVOL-EAYLFTESWRNMOAY-----A 208
DB 198 QPPQVSVAPLSTNLAING---SPTSKEITLPSVKAPESTLLETPENNNTSKINDTGS 254
QY 209 TEATTSAEAT--TPTPVATASASELAEHFTFPMLENGVDHYEPTP 253
DB 255 TTATTTATETEIKPEEDATPAS-LHODHYLVYNOR-ANHSKDP 299

RESULT 6
US-09-813-153-138
Sequence 138, Application US/09813153
Publication No. US20030045459A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: P2023
CURRENT APPLICATION NUMBER: US/09/813,153
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US/09/363,044
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,167
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,162
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,161

; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: PatentIn version 3.0.0

```

QY 100 SVFVGCKVTEY-----TFSASNRLTGPH-----PEKLTIRNRPNDSGMFYIVRL 146
    :: :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
Db 56 AVFPAPETISIMRLVTA-----GLPHEIIPVAGPIPHMLTKRAEGNET-----KF 102

```

QY 147 DDTKEPIDVFAIQL---SVYQFANTAATRGLYSKASCRTGFLPTVQLEA-YLRTEESWRN 202

Db 103 KDSMPDLVSQLATLRDLVYRAEDAAVLLG-----NIPSIAPAMFVYVRSRL 155
 QY 203 KQAYVATATTTSA-----EATPTPTAT-----ASELEAHEFTPEMLGVHD 248
 Db 156 YHPHVKAIAATGAALRAVIRLOAATSPDALIVAEEIFATGLKPGWVE----- 210
 QY 249 YEPTRANENSVYRLGTMSPTLIGVVAAVSATIGLVISITVRNMCPTPHKLDTVS 308
 Db 211 -----GDLSPYV--AAARALIDSGYEVLTNKRRESLYVESESLIAS 252
 QY 309 QDDEERSQ--TRRSKRFEGMVACELNGADDESELEVAIYNPSA-----LSSPDSI 360
 Db 253 YSTPGKOGVNMRESFTAGFLAAS--NDCKSTEDSVINAVAYANAGSEMDVITPTPKL 310
 QY 361 K 361
 Db 311 R 311

SUOL 9
 Sequence 1, Application US/09753436
 Patent No. US20010029293A1
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Vazeux, Rosemay
 TITLE OF INVENTION: ICAM-Related Materials and Methods
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borcun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/753,436
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/382,289
 FILING DATE:
 APPLICATION NUMBER: US 08/487,113
 FILING DATE: 07-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,754
 FILING DATE: 05-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Joseph A., Jr.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 33282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
 TELER: 25-3856
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 347 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 30..547
 US-09-753-436-1

Query Match
 Best Local Similarity 23.3%; Pred. No. 2.8;
 Matches 69; Conservative 36; Mismatches 80; Indels 11; Gaps 15;

QY 103 VGCKVTEYTFSSNRLTGPPEPKL-----TIR-----NRPDSGMFYI 143
 Db 98 VVNCNGSQITGSSNITVYGLPERVELAPLPMPQVGOFTLRKCOVEGSPR--TSLIVYL 154
 QY 144 VRLLD-----TRKIDVFAIQLS-----VGFANTATRGLY 175
 Db 155 LRMEELSRQPAVEPEAEVATVLAARDHGAFESCRTLEMDOPQIGLVNTSAPROL- 213
 QY 176 SKASCRTEGLPTV--OLEA--YLRTESV-----RMQAVVA-----TEATTT 214
 Db 214 -----RTFLVPTPRLVAPRFLVETSWPVDCTLDGLFPASEAQVYALGDMQMLATVM 268
 QY 215 SAATPTPIPVYATSALEA-----EHFT--FPMLENGVHYEPTPAN 255
 Db 269 NHDITLTATATATAAAGEGARELVCNVTLGGERREARENITVRSFLGPTVNLSEPT-AH 327
 QY 256 ENSNVYRLGTMSPTLIGVVAAVSATIGLVISITVRNMCPTPHKLDTVSDD 311
 Db 328 EGSTVTV--SCMAGARQVITLDGVPAAAPGQ-----TAQLNLATRESDD 369

RESULT 10
 US-09-870-759-73
 Sequence 73, Application US/09870759
 Patent No. US2002017751A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 PRIOR FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 73
 LENGTH: 365
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-870-759-73

Query Match
 Best Local Similarity 4.9%; Score 91; DB 9; Length 365;
 Matches 76; Conservative 52; Mismatches 128; Indels 124; Gaps 19;

QY 50 TQDLTFMPGQRPBKR-----YSGTVRV-----ARSDITNOGY 83
 Db 15 TQSL-----AHPHQIDILANTCRAGVHEKNGRYSISRTREADLCOAFNSTLPTMDQ 69
 QY 84 QELS-EERFENC-----THRSSVVGKAYE-----YFFSSNN 117
 Db 70 KMLASKGFEFCRYGTEGNNVYIPRIHNAICANHGYIILVTSNTSHYDTFCFENS-- 127
 QY 118 LTGPPEPKLIRN-PRPDSCMFYIVRLDTR-----EPIDVAIQLSYVGP 165
 Db 128 --APPEEDCYSYDLPSNDFGPTVTTIVNRDGTYSKKEGYRHOBDIDASN-----I 179

QY 166 ANTAATRGTSKASCRFTGLPTVOLAEYLTREESMRNM-----QAVVATEATTSAEAT 219
Db 180 DDVVSSSTTEKSTPEYILHT-----YLPTEQPTGDQDSFTRSLATRDSDSSDR 234
QY 220 TTPPVATSASEDAEHFTFPLWGVNDHYEPANENSNTVRLGTMSFPLIG---VTV 276
Db 235 GSSR-TVTHGSEL-AGH-----SSANDSCVTTTSCGPMRRPQIPEWILIL 277
QY 277 AAVVSATIGVIVISTYTRMCTPHRKLDVYSDODDERSTRESRKGPMVACEINKGA 336
Db 278 ASLALALILAVCIANSRRCOKKL--VINGNGTVEDRKP-----ELNGEA 326
QY 337 DQSELVELVAIVNPALSPP 358
Db 327 SKQSEMYHL---VNKPERSTPD 345

RESULT 11
US-09-978-295A-45
Sequence 45, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704


```

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085697
Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred No.2,4; Mismatches 113; Indels 117; Gaps 16;
Matches 72; Conservative 41;

5 LGTL---ALATLAPFGAMGIVTGNHVARLIDDIHVIYVAPRENTILOLF-----55
16 LGVLWVACMLLAASFETLOCBGPVCT--BESSCHTEDD---LTDAREAGFVKVATYTESP 70
56 -----FMGQPHKP--YSGTVVAFRSIDITNOCYQELSERFNCNCHSSSVFGCK 106
71 FHLIVSYDWLTLQCPAKPFVEDLVL---LRCQAMOD-----WP 106
107 VREYTFASNRLTGPMPH---FKLIRNRPNDGSMFY-----YIVR 145
107 LGQVTFYDGSALCPGPNREFSITV--VQKADSGHCSGITQSPGPGIETASVVAIT 164
146 LDD-----TKEPIDVFAIDL--SVYQFANTATNGLYSK 177
165 VOELFPAPILRAVPSAPQAGSPMLSCOTKLPQRSARLRFSPKDGRIVQSGLSSE 224
178 ASCTRFGLPTVQ-----LEAYLRTESMR--NMQAVVATEATTSAEATTPPVATTS 228
225 -----FQIPTASEDHSGSYWCEATEDNQWKSPOLEIRVOGASSA-----APPLTNP 274
229 ASLEAEHHTPPMLENGVDHYEPTPANENSNTVGLTMSPTL 271
275 APQKSAAPGTAPAEAPGPPLPPTPSSSDPGSSPLGMPDHL 317

RESULT 12
US-09-978-697-45
Sequence 45; Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin F.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
```

PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082566	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082766	PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083366	PRIOR FILING DATE: 1998-04-27	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083456	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083588	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05	PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-13
-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------	-------------------------------------	-------------------------------

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4; 113; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches

5 LGTL---ALIAATLAPGAGCIVITGNHVSARIDDIYIVAPREATIQLQLF-----55
16 LGVLMVAMQMLLASFTLOCEBPVCT-ESSCHTEDD---LTDAREAGFOVKATITSEP 70
56 -----FMFGQRPKRP-YSGTVVAFRSDITNOCYQELSEERFENCTHSSSVYGVCK 106
71 FHLIVSYDWLTLQSPKAPVFEGLLY-----LRQAMQD-----WP 106
107 VTEYFSASNRLTGPPHP---FKLTIIRNRPNDGMY-----VIVR 145
107 LQVTFYRDSGSLGPPGPNHRSITV--VQKADGHHGCSGIFQSPGPIPTASVAIT 164
146 LDD-----TREPIDVAIQL--SVYQFANTATGELSK 177
165 VOELFPAPILRAVPSAPQASPMILSCOTKILPORSAAALILSPFKDRIYQSGLSSE 224
178 ASCRFFGPTVQ-----LEAYLREESNR-IMQAVVATEATTSAETTPVTATTS 228
225 -----FOIPFASDEHSSGYCEAATEDNQVWQSPQLEIRQASASSA-----APPLTNP 274
229 ASELEAHEFTFPMLENGVDHYEPTPANENSNTVVLGTMSPTL 271
275 APOKSAFGTAPEARPGPLRPPTPSSEDPGSSPLGMPDPL 317

Db 165 VOELFPAPILRAVPSAPQASPMILSCOTKILPORSAAALILSPFKDRIYQSGLSSE 224
Db 178 ASCRFFGPTVQ-----LEAYLREESNR-IMQAVVATEATTSAETTPVTATTS 228
Qy 107 VTEYFSASNRLTGPPHP---FKLTIIRNRPNDGMY-----VIVR 145
Qy 107 LQVTFYRDSGSLGPPGPNHRSITV--VQKADGHHGCSGIFQSPGPIPTASVAIT 164
Qy 146 LDD-----TREPIDVAIQL--SVYQFANTATGELSK 177
Db 165 VOELFPAPILRAVPSAPQASPMILSCOTKILPORSAAALILSPFKDRIYQSGLSSE 224
Qy 178 ASCRFFGPTVQ-----LEAYLREESNR-IMQAVVATEATTSAETTPVTATTS 228
Db 225 -----FOIPFASDEHSSGYCEAATEDNQVWQSPQLEIRQASASSA-----APPLTNP 274
Qy 229 ASELEAHEFTFPMLENGVDHYEPTPANENSNTVVLGTMSPTL 271
Db 275 APOKSAFGTAPEARPGPLRPPTPSSEDPGSSPLGMPDPL 317

RESULT 13
US-09-978-192A-45
Sequence 45, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Wei-Qiang
APPLICANT: Geider, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070

```

: PRIOR FILING DATE: 1998-04-08
: PRIOR APPLICATION NUMBER: 60/081049
: PRIOR FILING DATE: 1998-04-08
: PRIOR APPLICATION NUMBER: 60/081071
: PRIOR FILING DATE: 1998-04-08
: PRIOR APPLICATION NUMBER: 60/081195
: PRIOR FILING DATE: 1998-04-08
: PRIOR APPLICATION NUMBER: 60/081203
: PRIOR FILING DATE: 1998-04-09
: PRIOR APPLICATION NUMBER: 60/081229
: PRIOR FILING DATE: 1998-04-09
: PRIOR APPLICATION NUMBER: 60/081955
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/081817
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/081819
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/081952
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/081838
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/082568
: PRIOR FILING DATE: 1998-04-21
: PRIOR APPLICATION NUMBER: 60/082569
: PRIOR FILING DATE: 1998-04-21
: PRIOR APPLICATION NUMBER: 60/082704
: PRIOR FILING DATE: 1998-04-22
: PRIOR APPLICATION NUMBER: 60/082804
: PRIOR FILING DATE: 1998-04-22
: PRIOR APPLICATION NUMBER: 60/082700
: PRIOR FILING DATE: 1998-04-22
: PRIOR APPLICATION NUMBER: 60/082797
: PRIOR FILING DATE: 1998-04-22
: PRIOR APPLICATION NUMBER: 60/082796
: PRIOR FILING DATE: 1998-04-23
: PRIOR APPLICATION NUMBER: 60/083336
: PRIOR FILING DATE: 1998-04-27
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/083392
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083495
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083496
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083499
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083545
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083554
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083558
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083559
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083500
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: 60/083742
: PRIOR FILING DATE: 1998-04-30
: PRIOR APPLICATION NUMBER: 60/084366
: PRIOR FILING DATE: 1998-05-05
: PRIOR APPLICATION NUMBER: 60/084414
: PRIOR FILING DATE: 1998-05-06
: PRIOR APPLICATION NUMBER: 60/084441
: PRIOR FILING DATE: 1998-05-06
: PRIOR APPLICATION NUMBER: 60/084637
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/084639
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/084640
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/084598
: PRIOR FILING DATE: 1998-05-07

```

```

: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/084627
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/084643
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/085339
: PRIOR FILING DATE: 1998-05-13
: PRIOR APPLICATION NUMBER: 60/085338
: PRIOR FILING DATE: 1998-05-13
: PRIOR APPLICATION NUMBER: 60/085323
: PRIOR FILING DATE: 1998-05-13
: PRIOR APPLICATION NUMBER: 60/085582
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085700
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085689
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085580
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085573
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085704
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085697

```

```

Query Match 4.9% Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches 113;

```

```

QY 5 LGTL-----ALTAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATLOLQF-----55
DB 16 LGVLWVAQMLNLAASFETLQCEGPVCT-ESSCHTEDD-----LTDAREAGHYVAYFESSE 70
QY 56 -----FMPGCRPHK-P-YSGTVRYAFRSDITNOCYQELSEREFNCJHKSSVYVGCK 106
DB 71 FHLIVSYDWLLILOGPAKPVFEGDLV-----LRCQAMOD-----NP 106
QY 107 VPEYTESASNRLLGPPHP---FKLTIRNRPNDSGMFY-----VIVR 145
DB 107 LTQVITYRQDGSALGPPGPNRERSITV--VOKADSGHYHSGIFQSGPCGIPETASVVAIT 164
QY 146 LDD-----TKEPIDVFAIOL--SVYQFANTAATRLGYEK 177
DB 165 VQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQKSAARLLFSFYKDGRIYQSRGLSSE 224
QY 178 ASCRFTGLPTVO-----LEAYLFTRESWR-NMQAYVATEATTTSAAETTPPTATIS 228
DB 225 -----FOIPTASEDHSGSYWCEATEDNOVMKOSPQLEIRVOGASSSA-----APPTLNP 274
QY 229 ASELAEHFTEFPLWENGVDHYEPTPANENSNVYRLGTMSPTL 271
DB 275 APOKSAAPGTAPAEADGPLPPPTPSSEDPGRSSPLGMPDPHL 317

RESULT 14
US-09-999-832A-45
Sequence 45, Application US/099999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC3
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: us/09/999,832A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077991
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085382
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;

Best Local Similarity 21.0%; Pctid No. 2.4; Indels 117; Gaps 16;

Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

QY 5 LGTL---ALLAATLAFGAMGIVITGNHVSARIDDDHIVAPREATTIQLF-----55
DB 16 LGVLMVAQMLLAASFETLCEGPVCT--EESCHTEDD---LTDAREAGQVAVATPSEP 70
DB 56 -----FMPGQRPKHP-YSGTVRAVAFRSDITNOCYQELSEERFENCCTHRSSSVFVCK 106
DB 71 FHLIVSYDWLILGQPAKPVVEGDLV-----LRCQAMQD-----WP 106
QY 107 VTEYTFASRLTGPHP---FKLITRNPRNDGMPY-----VIVR 145
DB 107 LTOVTTYRDSALGPEPNEFSITV--VOKADSGHHCIGTOSGPGTIPETASVAIT 164
QY 146 LDD-----TKEPIDVFAIOL--SVYQFANTATRGLYSK 177
DB 165 VQELFAPILRAVPSAEPQGSMTLSCQTKLPLQSAARLLFSFKDGHIVQSGRSLSE 224
QY 178 ASCTRTGLPVQ-----LEAVYLTREESMR-NMQAVYVTEATTTSAEATTPPYATIS 228
DB 225 -----FOIPTASEDHSGSYWCEATNEDNQWKOSPOLEIVQGASSA-----APPLNP 274
QY 229 ASLEAEHFTFPLWLVGVDHTEPTPANENSNVTVRLGTMSPTL 271
DB 275 APOKSAAPGTAPEDAPRLPPPTPSEDEPGFSSPLGMPDPL 317

RESULT 15
US-09-978-189-45
; Sequence 45, Application US/09978189

;; Publication No. US20030004102A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James:
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630PIC7
;; CURRENT APPLICATION NUMBER: US/09/978,189
;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078004
;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663

OY 178 ASCRTEGLPTVO-----LEAYLRTEESWR-NMOAYVATEATTTSABATTPPYTATS 228
Db 225 -----FOIPTASEDHSGSYWCCEATEDNOYWKOSPQLEIRVOGASSSA-----APPTLNP 274
OY 229 ASELEAHEFTFPWLENGVDHTEPTPANENSNTVRLGTMSPTL 271
Db 275 APQKSAAPGTAPEEAPGPLPPPTSSDDPGFSSPLGMPDPHL 317

Search completed: May 5, 2003, 16:26:32
Job time : 18.5 secs

PT methods of distinguishing between vaccinated and naturally infected
PT birds
XX
PS Example 1; Page 102-103; 177pp; English.
XX
CC The gi gene, spanning nucleotides 9874-10962 of the unique short
CC region (AAT33504) of infectious laryngotracheitis virus (ILT),
CC codes for a glycoprotein (AAM0635) of approx. 39,753 mol.wt.
CC The gi glycoprotein is homologous to Varicella-zoster gi.
CC Deletion of the gi gene results in an attenuated ILTV that
CC is useful as a vaccine against ILT disease in chickens.
CC Recombinant virus deleted for gi was safe in animal trials.
CC Deletion of the gi gene serves as a negative marker to
CC distinguish vaccines from infected animals. A gene coding
CC for a foreign antigen may be inserted into the gi gene to
CC produce a recombinant multivalent vaccine.
XX
SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 16; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATTIQLDFMPGQ 60
DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATTIQLDFMPGQ 60
OY 61 RPHKPYSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCATYETTFASNRITG 120
DB 61 RPHKPYSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCATYETTFASNRITG 120
OY 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
DB 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
OY 181 RTFGLPTVLEAVLRTREESRMQAVVATEATTSAETTPVTATSSASELAEHHTP 240
DB 181 RTFGLPTVLEAVLRTREESRMQAVVATEATTSAETTPVTATSSASELAEHHTP 240
OY 241 WLENGVDHYEPPPANENSNTVRLGTMSPLLIGTVAAVVSATIGLIVISITRNKCP 300
DB 241 WLENGVDHYEPPPANENSNTVRLGTMSPLLIGTVAAVVSATIGLIVISITRNKCP 300
OY 301 HRKLDIVSODDERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
OY 361 KM 362
DB 361 KM 362

RESULT 2
AAM06787
ID AAM06787 standard; Protein; 362 AA.
XX
AC AAM06787;
XX
DT 02-JUN-1997 (first entry)
XX
DE ILTV glycoprotein gi.
XX
KM ILTV; vaccine; vector; attenuation; poultry;
KM avian infectious bronchitis virus; Newcastle disease virus;
KM infectious bursal disease virus of chickens;
KM Marek's disease virus; herpesvirus; glycoprotein gi.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= sig-peptide 23..362

PT
FT Region /label= Mat_protein
FT 272..292
XX /label= Transmembrane_helix
XX
PN MO9629396-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US03916.
XX
PR 06-JUN-1995; 95US-0468190.
PR 23-MAR-1995; 95US-0410121.
XX
PA (SYTR) SYNTRO CORP.
XX
PI Cochran MD, Wild MA;
XX
DR WPI; 1996-443172/44.
DR N-PSDB; AAT44384;
DR N-PSDB; AAT44385.
XX
PT Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G₁ or us2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
XX Example 11; Page 110-111; 216pp; English.
XX
XX Glycoprotein gi (AAM06787) is encoded by ORF8 of the unique short
CC region (AAT44384) of infectious laryngotracheitis virus (ILT). It
CC shows homology to the Varicella zoster virus gi glycoprotein.
CC Recombinant ILTV gi protein produced in a swinepox virus reacts to
CC convalescent sera from ILTV-infected chickens. Deletion of the gi
CC gene results in an attenuated ILTV that is useful as a vaccine and
CC as a negative marker to distinguish vaccinees from infected
CC animals. Insertion of a foreign gene into the gi gene allows
CC prodn. of multivalent vaccines.
XX
SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 17; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATTIQLDFMPGQ 60
DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATTIQLDFMPGQ 60
OY 61 RPHKPYSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCATYETTFASNRITG 120
DB 61 RPHKPYSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCATYETTFASNRITG 120
OY 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
DB 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
OY 181 RTFGLPTVLEAVLRTREESRMQAVVATEATTSAETTPVTATSSASELAEHHTP 240
DB 181 RTFGLPTVLEAVLRTREESRMQAVVATEATTSAETTPVTATSSASELAEHHTP 240
OY 241 WLENGVDHYEPPPANENSNTVRLGTMSPLLIGTVAAVVSATIGLIVISITRNKCP 300
DB 241 WLENGVDHYEPPPANENSNTVRLGTMSPLLIGTVAAVVSATIGLIVISITRNKCP 300
OY 301 HRKLDIVSODDERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
OY 361 KM 362
DB 361 KM 362

RESULT 3

XX	AAW11475;
XX	30-APR-1997 (first entry)
XX	Marek's disease virus glycoprotein gI.
XX	MDV; UL32; membrane glycoprotein 82; glycoprotein gI; antigen;
XX	vaccine; vector; fowlpox virus.
XX	Marek's disease gammaherpesvirus type 1 strain GA.
XX	MO9703187-A2.
XX	30-JAN-1997.
XX	05-JUL-1996; 96WO-US11360.
XX	07-JUL-1995; 95US-0499474.
XX	(JARG) NIPPON ZEON KK. (USDA) US SEC OF AGRIC.
XX	Lee LF, Nazarian K, Wilter RL, Wu P, Yanagida N; Yoshida S; WPI. 1997-119044/11.
XX	New DNA encoding glycoprotein 82 of Marek disease virus - useful in PT vaccines to protect poultry
XX	Disclosure; page 72-73; 101ip; English.
XX	Genes encoding Marek's disease virus glycoprotein gI (AAW11475) and/or glycoprotein gE (AAW11474) can be incorporated into recombinant viral vectors that also carry the UL32 gene (see also CC AAU51358) encoding glycoprotein 82 (AAW11473). The gI and gE genes were cloned from MDV genomic DNA by PCR (see also AAU51368-69 and CC AAU51365-67). A transfer vector was constructed that was used to produce a recombinant fowlpox virus useful as a vaccine to protect poultry against MDV infection.
XX	Sequence 355 AA:
SO	
Query Match	8.2%; Score 152; DB 18; Length 355;
Best Local Similarity	22.9%; Pred. NO. 3.5e-06;
Matches 78;	Conservative 55; Mismatches 166; Indels 42; Gaps 14
OY	19 GAMGIVITGNHNSAKIDDDHIYVARRP-ATIQLOLFMPQGPRIKPSGVIRVAFRSD 77.
Db	15 GIWSIVYGTSTLTSLDSDALAFGLCKMNVNRQLLELGDOTRTSSVTGETEI.LKWD 73
OY	78 ITNOCYQELSEERFENCTHRSSSVFGCKVTEYTESASNLRCGPHPRK---LTRINRR 134
Db	74 EYKKCYISVLHARSYNDCAIDAIVTRGCDAVVYAQRDRV--QPREPGTLLRIYEPKV 131
OY	135 NDSCGFVIYIVRLDTKEPIDIVAIGLSVYOAFANTAAIRGLYSKASCRTGFLPTVOLEAVL 194
Db	132 SDTGSIYIRVALAG-RNMKDIFRMAYIIRS-----SKSMACNHSASFQAHKCI 179
OY	195 RTEE--SNRNMQAVYATEHTTSASEATTPTPYTATSASFLEAHNFPPYLENGVDHYDEPT 252
Db	180 RYVDMMAEEENTLIGVGNLDSODELHAIVNTTPDIS-TDINIITTPPYDNGSTIYSP 238
OY	253 P---ANEKSNTYVRIGT-MSPTLIQGYTAADV--SATIGLVIV--ISIVTRNMCTPHRK 303
Db	239 VFENLENNSHVADAMSTGMWMTVLKATLPRLIYFSMIYLICIAIALIYLCERCSCRPHRR 298
OY	304 LDTVSQDODEBSQTRRESKRKFGPMVACETLNKCADDSELVE 344

	Db	299	I----	YIGEPKRSDE-----APLITSVAVNESFYQDYNNKE	328
	-RESULT 6				
	ID	AAMW22999			
	Xx	AAW22999 standard; Protein:	364 AA.		
	Xc	AAW22999;			
	Dt	20-FEB-1998	(first entry)		
	Xx	Canine herpesvirus glycoprotein I PCgI364.			
	Kw	Vaccine; vector; gene therapy; canid; dog; CHV; Cgi; PCgI364;			
	Xx	glycoprotein I.			
	Ov	Canine herpesvirus.			
	Pn	WO9729772-A1.			
	Pd	21-AUG-1997.			
	Ef	14-FEB-1997;	'97MO-USO4115.		
	Xr	15-FEB-1996;	96US-O602010.		
	Pa	(HESK-) HESKA CORP.			
	Pi	Frank RA, Heanes EJ;			
	Dk	WP1; 1997-424758/39.			
	N-	N-PADB: AAT75616.			
	Rt	Recombinant canine herpes virus and its genome - useful as vaccine			
	Cc	to protect canids against infectious, metabolic or genetic diseases			
	Ss	Claim 57; Page 181-182; 240pp; English.			
	Cc	This protein comprises canine herpesvirus (CHV) glycoprotein I			
	Cc	((PgI364)). Its sequence was deduced from a coding region found in			
	Cc	CHV genomic DNA molecule ncus10592 (see AAT75616). PG1364 can be			
	Cc	expressed in transformed host cells. CHV proteins, nucleic acids,			
	Cc	and antibodies raised against CHV proteins, can be used to protect			
	Cc	candid aginstnt CHV infection. Novel recombinant CHV and novel			
	Cc	recombinant CHV genomes that contain heterologous nucleic acid			
	Cc	molecules inserted e.g. Into Cgi gene, can be used as vaccines to			
	Cc	protect candid against infectious, metabolic or genetic diseases.			
	Ss	Sequence 364 AA;			
	Query Match	7.9%.	Score 148;	Dl 18:	Length 364;
	Best Local Similarity	27.3%	Fred. No. 8.9e-06;		
	Matches	45; Conservative	30; Mismatches	82; Indels	8; Gaps
					4;
	Yy	4 LLGTLALLAATLPARGAGIVTGNHVARSRIDDDIHVIADPREATTLOLFMPGR-P	62		
	Db	16 LITMFLRILRLFLXGVNGFVKGYIMELNTSSGFIFPDCKRTVSGLLLFDGDHLIS	75		
	Oy	63 HKPSYGVAVRASRDITNOCYOELSERRFNCTHRSSSVENC--KTVEYTFASNRILT	G		
	Dy	76 VVNNSCYATEFI---HFNSSCVTVOTIEFYFCSPRIFFNAFPSCLEKKVSKHNHSOLIRINS	132		
	Oy	121 PRPHREKLTIINPRNDSGMFYVIALDTEKDIDVFALQLSYOR	L5		
	Dy	133 IEKVVLLETINKRPMDSGVTFRVOLENN-KTDVGIPARITYSR	175		
	RESULT 7				
	ID	AAMW2659			
	Xx	AAW2659 standard; Protein:	364 AA.		
	Xc	AAW2659;			
	Xx				

```

DT 07-JAN-1999 (first entry)
XX
XX Canine herpes virus protein sequence PC91-364.
DE
XX Canine herpes virus; CHV; recombinant canine herpes virus vector;
XX genome; vaccination; dog; protozoan; helminth; ectoparasite; bacteria;
XX virus infection.
XX
XX Canine herpes virus.
OS
XX
XX US5804197-A.
XX
XX 08-SEP-1998.
XX
XX 12-JUL-1996; 96US-0680726.
XX
XX 12-JUL-1996; 96US-0680726.
XX
XX 13-FEB-1996; 96US-0602010.
XX
XX (HESK-) HESKA CORP.
XX
XX Frank RS, Haanes EJ;
XX WPI: 1998-505590/43.
XX N-PSDB; AAV66941.
XX
XX Canine herpes virus nucleic acids - useful for producing recombinant
XX canine herpes virus vectors
XX
XX Claim 7; Column 133-136; 103pp; English.
XX
XX The present sequence represents a canine herpes virus (CHV) protein
XX used for DNA vaccination of dogs against CHV and also other infective
XX agents such as protozoan, helminths, ectoparasites, bacteria and
XX viruses. CHV can be formulated by incorporation of heterologous nucleic
XX acid molecules as a single multivalent therapeutic composition against
XX a variety of canine pathogens.
XX
XX Sequence 364 AA;
XX
XX Query Match 7.9%; Score 148; DB 19; Length 364;
XX Best Local Similarity 27.3%; Pred. No. 8.9e-06;
XX Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
XX
XX 4 LGCTLALAAATLAPGAMGIVITGNHVSARIDDDHIVVAPRPATITOLDFPMPGCR-P 62
XX 16 LITIMFLPLFLFLVGVNGFYVKGTYISMLNTSSGFSIFPDDKFIYSGRLFLDDQHLN 75
XX
XX 63 HKPYSGTVAVAFRSDITNOCYOELESEEFENCTHRSSSVFVGC--KTEYTFASNRLTG 120
XX
XX 76 VNNYSCTIEFI--HNNSCITYVOTIEYFSCPRIFNNAFRSCCLKVSKHESQLINNS 132
XX
XX 121 PPHPFKLTIRNRPNDSCGMFYVIRLDDTKREPIDVFAIOLSYOF 165
XX
XX 133 IENGVLLEITNRPNDSCGMFYVIRVLENNK--TDVGFIPAFIYSF 175
XX
XX
XX RESULT 8
XX AAB51316
XX ID AAB51316 standard; Protein; 364 AA.
XX
XX AAB51316;
XX
XX 29-MAR-2001 (first entry)
XX
XX Canine herpes virus protein sequence SEQ ID NO:56.
XX
XX Canine herpes virus; CHV; antiallergic; immunosuppressive; cytostatic;
XX antibacterial; antiinflammatory; vaccine; candid; infectious disease;
XX genetic disease; metabolic disease; abnormal cell growth; allergy;
XX degenerative process; immunological defect; autoimmune disease; cancer;
XX cardiovascular disease; graft rejection; hematopoietic disorder;

```

```

XX
XX immunodeficiency disease; immunoproliferative disease; septic shock;
XX immunosuppressive disorder; inflammatory disease; jaundice.
XX
XX Canine herpes virus.
OS
XX
XX US6159478-A.
XX
XX 12-DEC-2000.
XX
XX 29-JAN-1998; 98US-0092409.
XX
XX 12-JUL-1996; 96US-0680726.
XX
XX 15-FEB-1996; 96US-0602010.
XX
XX (HESK-) HESKA CORP.
XX
XX Frank RS, Haanes EJ;
XX WPI: 2001-090270/10.
XX N-PSDB; AAF26761.
XX
XX Novel recombinant canine herpes virus protein useful for protecting
XX animals, in particular candid from herpes virus infection and various
XX diseases including cancer and autoimmune diseases
XX
XX Example 10; Column 135-136; 101pp; English.
XX
XX The present invention describes an isolated canine herpes virus (CHV)
XX (i) CDUTPase protein encoded by a CHV nucleic acid molecule that
XX hybridises under stringent hybridisation conditions with the CDUTPase
XX gene. Also described is a therapeutic composition (ii) comprising (i),
XX (1) has antiallergic, immunosuppressive, cytostatic, antibacterial and
XX antiinflammatory activities, and can be used in vaccines. (1) is useful
XX for protecting an animal, in particular a candid from CHV. Therapeutic
XX compositions comprising (1) are used for treating infectious diseases,
XX genetic diseases and other degenerative processes and/or
XX immunological defects including allergies, autoimmune diseases,
XX cancers, cardiovascular diseases, graft rejection, hematopoietic
XX disorders, immunodeficiency diseases, immunoproliferative diseases,
XX immunosuppressive disorders, inflammatory diseases, jaundice, and septic
XX shock. CHV need not be attenuated for use as a live vaccine vector due
XX to the low pathogenicity of natural CHV, particularly as compared to
XX AAB51327 represent CHV nucleotides, proteins and PCR primers used in the
XX exemplification of the present invention.
XX
XX Sequence 364 AA;
XX
XX Query Match 7.9%; Score 148; DB 22; Length 364;
XX Best Local Similarity 27.3%; Pred. No. 8.9e-06;
XX Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
XX
XX 4 LGCTLALAAATLAPGAMGIVITGNHVSARIDDDHIVVAPRPATITOLDFPMPGCR-P 62
XX 16 LITIMFLPLFLFLVGVNGFYVKGTYISMLNTSSGFSIFPDDKFIYSGRLFLDDQHLN 75
XX
XX 63 HKPYSGTVAVAFRSDITNOCYOELESEEFENCTHRSSSVFVGC--KTEYTFASNRLTG 120
XX
XX 76 VNNYSCTIEFI--HNNSCITYVOTIEYFSCPRIFNNAFRSCCLKVSKHESQLINNS 132
XX
XX 121 PPHPFKLTIRNRPNDSCGMFYVIRLDDTKREPIDVFAIOLSYOF 165
XX
XX 133 IENGVLLEITNRPNDSCGMFYVIRVLENNK--TDVGFIPAFIYSF 175
XX
XX
XX RESULT 9
XX AAP70645
XX ID AAP70645 standard; Protein; 350 AA.
XX
XX AAP70645;
XX
XX 29-APR-1991 (first entry)
XX

```

```

XX DE Pseudorabies virus gp63 protein.
XX KM PRV; vaccine; GI: gp50; gp63.
XX OS Pseudorabies virus.
XX PN W08702058-A.
XX PD 09-APR-1987.
XX PF 28-AUG-1986; 86WO-US01761.
XX PR 16-JUL-1986; 86US-0886260.
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 26-MAR-1986; 86US-0844133.
XX PA (UPJO ) UPJOHN CO.
XX PA (PETR/) PETROVSKIS E A.
XX DR Petrovskis EA, Post LE, Timmins JG;
XX DR WPI: 1987-108699/15.
XX DR N-PSDB; AAN70994.
XX PT Pseudo-rabies virus protein - produced from recombinant DNA and
XX PT used to produce vaccine and detect animals infected with virulent
XX PT virus.
XX PS Claim 8; Page 59; 67pp; English.
XX CC The PRV glycoprotein product may be used as in vaccination of
XX CC animals such as swine, sheep and goats against infection by the
XX CC virus. The protein may be produced from a transfected expression
XX CC system such as E.coli, yeast or CHO cells operatively linked to a
XX CC suitable expression control sequence. Glycoproteins gp1 and gp63 may
XX CC be used to distinguish between infected and vaccinated animals.
XX CC See also AAN70993-5.
XX SQ Sequence 350 AA;
XX
XX Query Match 7.7%; Score 143.5; DB 8; Length 350;
XX Best Local Similarity 22.8%; Pred. No. 2.3e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX QY 8 LALLAATLAFPGAM--GIVITGNHVSARIDDDHIVVAPRPEATIQQLFPMGQRRHKP 65
XX DB 15 LLLAALTLAALTPRVGVLFRGAGSVHAGSAVLVPGDAPNLTIDGTLFLFGSPSPN- 73
XX QY 66 YSGTVRAFRSDITNOCYQELSEERFENCNHRSSSVFVC--KVTEYTFGAS-----NRL 118
XX DB 74 YSGRVEL-LRLDPRKACYTREYAEYDLCPRVHHEAFRGCLRKEPLARRASAAVEARRL 132
XX QY 119 TGRPHFKLIRNPRNDSGMFYVIRLDTPKEPIDVFAQLSVYQFANAAATRG----- 174
XX DB 133 -----LFSVRPAPPDAGSYLVLRVNGT---TDLFVLTALV-----PPRGPRHP 174
XX QY 175 --YSKASCRTEFGFLPTVQLEAYLRTESWRMMAVY--ATEATTSA-----EATPTPV 224
XX DB 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVTA 277
XX DB 222 RGTGAPRPEPSDEEDE-----EGATJAMTPVPETLDANGM---VNASVSVLL 271
XX QY 278 AVVSATIG-----LVYISIVTRNMCTPHKRLDIVSODDERSCOTRRESRK 323
XX DB 272 AANAATAGARGPKIAMVGLPTIVLLIFLGVACAARCARCARGIASTGRDPCGAARSTR 331
XX RESULT 10

```

```

AAR63143
XX ID AAR63143 standard; Protein: 350 AA.
XX AC AAR63143;
XX DT 12-JUN-1995 (first entry)
XX DE Glycoprotein 63 (gp63) of pseudorabies virus.
XX KM Pseudorabies virus; PRV; glycoprotein; gp50; GI: gp63;
XX KM determination; detection; vaccine; infected animal; isolation;
XX KM cloning; virulence.
XX OS Pseudorabies virus.
XX PN US5352575-A.
XX PD 04-OCT-1994.
XX PF 04-OCT-1985; 85US-0784787.
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 16-JUL-1986; 86US-0886260.
XX PR 29-JUN-1987; 87US-0100817.
XX PR 20-APR-1990; 90US-0513282.
XX PA (UPJO ) UPJOHN CO.
XX PA Petrovskis EA, Post LE, Timmins JG;
XX PT WPI: 1994-316176/39.
XX PT N-PSDB; AAO73489.
XX PT Identifying animals vaccinated against pseudorabies virus - by
XX PT detecting the absence of GI or GP.63 antibodies in serum to
XX PT distinguish vaccinated from infected animals
XX PS Example 3; Column 21-24; 21pp; English.
XX CC AAR63143 shows the protein sequence of gp63 (glycoprotein) encoded by
XX CC AAO73489, isolated from Pseudorabies virus (PRV). The DNA and protein
XX CC sequences of the invention are useful in a method for distinguishing an
XX CC animal vaccinated with a PRV vaccine lacking glycoprotein GI, GP63 or
XX CC GP50 from an animal infected with a virulent wild-type PRV without
XX CC sacrificing the animal. The method is used to test animals such as
XX CC swine, cattle, sheep and goats. (see AAR63142 and AAR63144).
XX SQ Sequence 350 AA;
XX
XX Query Match 7.7%; Score 143.5; DB 15; Length 350;
XX Best Local Similarity 22.8%; Pred. No. 2.3e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX QY 8 LALLAATLAFPGAM--GIVITGNHVSARIDDDHIVVAPRPEATIQQLFPMGQRRHKP 65
XX DB 15 LLLAALTLAALTPRVGVLFRGAGSVHAGSAVLVPGDAPNLTIDGTLFLFGSPSPN- 73
XX QY 66 YSGTVRAFRSDITNOCYQELSEERFENCNHRSSSVFVC--KVTEYTFGAS-----NRL 118
XX DB 74 YSGRVEL-LRLDPRKACYTREYAEYDLCPRVHHEAFRGCLRKEPLARRASAAVEARRL 132
XX QY 119 TGRPHFKLIRNPRNDSGMFYVIRLDTPKEPIDVFAQLSVYQFANAAATRG----- 174
XX DB 133 -----LFSVRPAPPDAGSYLVLRVNGT---TDLFVLTALV-----PPRGPRHP 174
XX QY 175 --YSKASCRTEFGFLPTVQLEAYLRTESWRMMAVY--ATEATTSA-----EATPTPV 224
XX DB 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVTA 277
XX DB 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVTA 277

```

```

DB 222 RGTGATPEPRSDDEEED-----EGATTANTPVPGTLDANGTM--VLNASVSRVL 271
OY 278 AVSATIG-----LVIVISIVTRNMCTPHKLDTVSODDEBSQTRRESRK 323
DB 272 AAANATGARGPGKIAMVIGPTIVLLIFLGVAACARCAARGIASTGRDPAARRSTR 331

RESULT 11
AAE05396
ID AAE05396 standard; Protein: 350 AA.
AC AAE05396;
XX
XX 24-SEP-2001 (first entry)
DE Pseudorabies virus (PRV) glycoprotein gp63.
XX Pseudorabies virus; PRV; glycoprotein; gp63; immunostimulant; vaccine;
XX PRV infection.
XX Pseudorabies virus.
XX
XX Key Location/Qualifiers.
FH Misc-difference 131 /note- "Encoded by GCG"
FT Misc-difference 132 /note- "Encoded by GTG"
FT Misc-difference 144 /note- "Encoded by GCG"
FT Misc-difference 207 /note- "Encoded by GCG"
FT Misc-difference 222 /note- "Encoded by GCG"
FT Misc-difference 223 /note- "Encoded by GCG"
FT Misc-difference 284 /note- "Encoded by GCG"
FT Misc-difference 334 /note- "Encoded by GCG"
FT Misc-difference 334 /note- "Encoded by GCG"
XX
XX US6261563-B1.
XX
XX 17-JUL-2001.
XX
XX 07-JUN-1995; 95US-0485287.
XX
XX 20-APR-1990; 90US-0513282.
XX 21-JUN-1994; 94US-0262813;
XX 28-AUG-1986; 86MO-0501761.
XX 26-NOV-1985; 85US-0801799.
XX 26-MAR-1986; 86US-0844113.
XX 16-JUL-1986; 86US-0886260.
XX 29-JUN-1987; 87US-0100817.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Petrovskis EA, Post LE, Timmins JG;
XX
XX WPI: 2001-450478/48.
XX
XX N-PSDB: AAD10195.
XX
XX Polypeptide comprising a pure and isolated pseudorabies virus gp63
XX polypeptide or its fragments, useful as a vaccine for protecting
XX animals against pseudorabies virus infection.
XX
XX Claim 1: Column 39-40; 21pp; English.
XX
XX The invention relates to pseudorabies virus (PRV) glycoproteins gp50,
XX gp63, gI and their corresponding DNA molecules. These glycoproteins are
XX used as vaccines for protecting animals against PRV infection.
XX The invention also relates to methods for protecting animals against PRV
XX infections and methods for distinguishing between infected and vaccinated
XX animals. The present sequence is pseudorabies virus (PRV) glycoprotein

```

```

CC 9p63.
XX
XX Sequence 350 AA:
SQ
Query Match 7.7%; Score 143.5; DB 22; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

OY 8 LALLAATLAPFGAM--GIVTGNHVSARIDDIHIVAVAPREPATIQLOLFEPGPRPKR 65
DB 15 LLLAALLAALPRVGVLFPRGACVSVHAGSVLVPGBAPMLTIDGTLLEBSPSPN- 73
OY 66 YSGTVAVAFRSDITNOCYOELEERFENCNRSSVFVC--KVETFEFAS-----NRL 118
DB 74 YSGRVEL-LRLDPKACVTRREYAEYDLCPRVHNEAFRCCLRKREPLARASAAVEARRL 132
OY 119 TGPRPHFKLITRPNRNSGMFVYIVRLDQTKREPIDVFALQLSYQFANPAATFGL---- 174
DB 133 -----LFVSRPAPRAGSYVLARVNGT---TDLFVLTALV-----PRGRPHR 174
OY 175 --YSKASCRFGLPVTVOLEALTRTESRWMAVY--ATEATTTS-----AEATPTPV 224
DB 175 TPSSADECR-----PVV-----GSMHSLAVVPADAVFTTPPIEPPTPAP 221
OY 225 TATSAS-----ELEAEHFTFPWLENGVDHYEPTPANENSIVYRLGTSMPILGYTA 277
DB 222 RGTGATPEPRSDDEEED-----EGATTAMTPVPGTLDANGTM--VLNASVSRVL 271
OY 278 AVSATIG-----LVIVISIVTRNMCTPHKLDTVSODDEBSQTRRESRK 323
DB 272 AAANATGARGPGKIAMVIGPTIVLLIFLGVAACARCAARGIASTGRDPAARRSTR 331

RESULT 12
AAR80637
ID AAR80637 standard; Protein: 317 AA.
XX
XX AAR80637;
XX
XX 21-DEC-1995 (first entry)
XX
XX Bovine herpes virus-1 mutant ORF1 product.
XX
XX BHV-1; vaccine; gIV gene; antigen.
XX
XX Bovine herpesvirus.
XX
XX EP663403-A1.
XX
XX 19-JUL-1995.
XX
XX 18-NOV-1994; 94EP-0203361.
XX
XX 23-NOV-1993; 93EP-0203274.
XX
XX (ALKU ) AKZO NOBEL NV.
XX
XX Kell G;
XX
XX WPI: 1995-247499/33.
XX
XX N-PSDB: AAQ9001.
XX
XX New bovine herpes virus with mutation in ORF1 and polyA signal for
XX gIV gene - useful as a vaccine, esp. where the mutation is insertion
XX of sequence encoding an heterologous antigen
XX
XX Claim 2: Page 13-14; 28pp; English.
XX
XX To produce a new BHV-1 mutant, DNA encoding gIV (flanked on both
XX sides by a sequence that allows homologous recombination) and a
XX host cell. Since the gIV-neg. virus cannot replicate, virus particles
XX are produced only when homologous recombination with the DNA has

```



```

XX 03-JUL-2001.
PD
XX 07-JUN-1995; 95US-0485289.
XX
XX 20-APR-1990; 90US-0513282.
XX 21-JUN-1994; 94US-0262813.
XX 28-AUG-1986; 86MO-US01761.
XX 26-MAR-1986; 86US-0844113.
XX 16-JUL-1986; 86US-0886260.
XX 29-JUN-1987; 87US-0100817.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Petrovskis EA, Post LE, Timmins JG;
XX
XX WPI: 2001-432046/46.
XX
XX N-PSDB; AAF90626.
XX
XX New recombinant DNA for screening animals actively infected with
XX pseudorabies virus (PRV), or for producing proteins useful as a vaccine
XX for protecting animals against PRV infection
XX
XX Example 3; Column 21-24; 21pp; English.
XX
XX The present sequence is that of pseudorabies virus (PRV)
XX glycoprotein gp63. The invention provides PRV gp50, gp63 and gI
XX glycoproteins (see AAB82501-03) and polynucleotides (see
XX AAF90625-27), and transformed host cells (especially CHO, yeast
XX and Escherichia coli) used to produce the polypeptides. Also
XX provided are subunit vaccines for PRV, methods for protecting
XX animals against PRV infection and methods for distinguishing
XX between infected and vaccinated animals. Commercial vaccines
XX have been found to have the gI and gp63 genes deleted. The gI and
XX gp63 polypeptides can therefore be used as diagnostic agents to
XX distinguish between animals vaccinated with these commercial
XX vaccines and those infected with the virulent virus.
XX
XX Sequence 350 AA:
SQ
Query Match 7.6%; Score 141.5; DB 22; Length 350;
Best Local Similarity 22.8%; Pred. No. 3.7e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
QY 8 LALLAATLAPFGAM--GIVITGNHVSARIDDDHIVAPREATIOLQLEFMPGQRPKRP 65
DB 15 LLLAALTLAALTPRGVGLFRGAASVHVAGSAVLVPGDAPRLTIDGTLFLLEGPSPSN- 73
Y YSGTVAVPRSDITNOCYOELSEERFENCNTHRSSVFVGC--KTEYEFSSAS-----NRL 118
DB 74 YSGRVGL-LRLDPKRCACYTRREYAEDLCPRVHNEAFRCGLKREPLARASAAVEARL 132
QY 119 TGPPIHFKLTIRNPRNDSGMFYIVRLDQTKREPIDVFALQLSYQFANTATPGL- 174
DB 133 -----LFVGRAPAPDAGSYVLRVAVNGT--TDLFVLTAIV-----PRGRPHR 174
QY 175 --YSKASCRFTGLPTVOLEAVLRTESRMWQAYV--ATEATTS-----AEATTPPV 224
DB 175 TPSSADECR---PYV-----GSMHSLAVVYPADAVFTTPPIIEEPPTTPAPR 221
QY 225 TATSAS-----ELEAHTFPLENGVDHYEPTPAAANSVYRLQTMSPILLIGTYA 277
DB 222 RCGCATPRGRSDEEBDE-----EGATTAMTPVGVGTIDANGT--VLNAAVSIVLL 271
QY 278 AVVSATIG-----LTVISIVTRMCTPRAKLLDYSQDDEESQTRRSRK 323
DB 272 AAAMATAGARGKTIAMVLPPTIVVLLIFGVACARACANGIASGTDRGAARSTRR 331

```

RESULT 15
AAR48063
ID AAR48063 standard; Protein: 380 AA.
XX

```

AC AAR48063;
XX
XX 20-JUL-1994 (first entry)
DT
XX
XX Sequence of polypeptide encoded by the first open reading frame in
DE the unique short (US) region of bovine herpes virus (BHV) genome.
XX
XX Insertion region; unique short region; US; vaccine; antigen.
XX
XX Bovine herpes virus type 1, strain ST.
XX
XX WO9400586-A.
XX
XX 06-JAN-1994.
XX
XX 25-JUN-1993; 93WO-FR00642.
XX
XX 26-JUN-1992; 92FR-0007930.
XX
XX (INMR ) RHONE MERIEUX SA.
XX
XX Audoumet JF, Legastelois ICMA, Leung-tack P, Riviere MEA;
XX
XX WPI: 1994-026222/03.
XX
XX N-PSDB; AA053350.
XX
XX New insertion region sequence of bovine herpes virus genomic DNA
XX used for recombinant viruses with this region deleted or
XX inactivated, useful in vaccines allowing differentiation between
XX vaccinated and infected cattle
XX
XX Claim 9; Fig 2; 47pp; French.
XX
XX The 4190 bp sequence in AA053350 encodes polypeptides homologous to
XX HSV-1 gI, gE and US9; these are neither essential for in vitro
XX replication nor important in inducing a protective immune response.
XX It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
XX known as infectious bovine rhinotracheitis virus.) The sequence
XX forms the insertion region in genomic DNA. BHV in which the
XX specific insertion region, esp. nucleotides 172-1311, has been
XX deleted or inactivated by insertion are claimed.
XX
XX Sequence 380 AA:
SQ
Query Match 7.5%; Score 140.5; DB 15; Length 380;
Best Local Similarity 25.3%; Pred. No. 5.2e-05;
Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
QY 1 MASLGTIALIATLAPFGAMGIVITGNHVSARIDDDHIVAPREATIOL-QLEFMP 58
DB 1 MRCILLMMVVILARAP--ARSLVYRGEAVGLRADGVAFVAPR-TDATALRGRLTFL 57
QY 59 GORP-HRPSGTVAVPRSDITNOCYOELSEERFENCNTHRSSVFVGC-KTEYEFSSASNR 117
DB 58 HQLEAGRRVNGVEL-LRYHAAGDCFVMLQTTAFASCPRVANNAFSCLDHDTPRASER 116
QY 118 LTGP--PHPRKLTIRNPRNDSGMFYIVRLDQTKREPIDVFALQLSYQFANTATPGL- 166
DB 117 RASAAVENHVLFIARPRIDSGVFLVAGVYGSTASERRRNVFLAFAVSTGEPPDP 176
QY 167 -----NTAATRGVSKASCRFTGL-----PTVOLEAVLRTESMR 201
DB 177 EAARTAPRSRGRPASGLTSSASLYDRALARPAPPPRPARPAAAGRRPERVE 236
QY 202 NMQAVVATEATTTSATTTPTVYTSAS 230
DB 237 TTEVDAATRAGSAFALTPPAGPTASPA 265

```

Search completed: May 5, 2003, 16:12:59
Job time : 54.5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:11:13 : Search time 19.5 Seconds
(without alignments)
546.210 Million cell updates/sec

Title: US-09-993-777-7
Perfect score: 1863
Sequence: 1 MASLIGTALLATLAPFGA.....VELVAIVPSALSSPSIKM 362

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5.

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1863	100.0	362	5	Sequence 7, Appl 1
2	1863	100.0	362	5	Sequence 68, Appl 1
3	152	9.2	385	4	Sequence 28, Appl 1
4	148	7.9	317	2	Sequence 2, Appl 1
5	148	7.9	364	1	Sequence 56, Appl 1
6	148	7.9	364	4	Sequence 10, Appl 1
7	145	7.7	310	3	Sequence 10, Appl 1
8	143.5	7.7	350	6	Sequence 2, Appl 1
9	140.5	7.5	380	4	Sequence 2, Appl 1
10	112	6.0	387	1	Sequence 63, Appl 1
11	108	5.8	713	4	Sequence 63, Appl 1
12	108	5.8	713	4	Sequence 63, Appl 1
13	108	5.8	713	4	Sequence 63, Appl 1
14	108	5.8	713	4	Sequence 63, Appl 1
15	108	5.8	713	4	Sequence 63, Appl 1
16	107.5	5.8	100	3	Sequence 27, Appl 1
17	107.5	5.8	100	3	Sequence 27, Appl 1
18	103.5	5.6	94	1	Sequence 6, Appl 1
19	103.5	5.6	94	1	Sequence 6, Appl 1
20	103.5	5.6	94	1	Sequence 6, Appl 1
21	103.5	5.6	94	1	Sequence 6, Appl 1
22	99	5.3	97	3	Sequence 25, Appl 1
23	98	5.3	503	1	Sequence 2, Appl 1
24	98	5.3	503	1	Sequence 2, Appl 1
25	98	5.3	503	1	Sequence 2, Appl 1
26	97	5.2	1220	2	Sequence 36, Appl 1
27	93.5	5.0	878	4	Sequence 2, Appl 1

28	93.5	5.0	907	3	US-08-783-774-2	Sequence 2, Appl 1
29	93.5	5.0	907	4	US-09-328-599A-1	Sequence 1, Appl 1
30	93.5	5.0	907	5	PCT-US96-03916-19	Sequence 19, Appl 1
31	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl 1
32	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl 1
33	92.5	5.0	547	1	US-08-433-010-1	Sequence 1, Appl 1
34	92.5	5.0	547	1	US-08-482-882-1	Sequence 1, Appl 1
35	92.5	5.0	547	2	US-08-483-383-1	Sequence 1, Appl 1
36	92.5	5.0	547	2	US-08-487-113D-1	Sequence 1, Appl 1
37	92.5	5.0	547	2	US-08-473-503-1	Sequence 1, Appl 1
38	92.5	5.0	547	2	US-08-483-932-1	Sequence 1, Appl 1
39	92.5	5.0	547	2	US-08-720-420A-1	Sequence 1, Appl 1
40	92.5	5.0	547	3	US-08-714-017-1	Sequence 1, Appl 1
41	92.5	5.0	547	3	US-08-863-790-1	Sequence 1, Appl 1
42	92.5	5.0	547	3	US-08-475-680-1	Sequence 1, Appl 1
43	92.5	5.0	547	4	US-08-296-749-1	Sequence 1, Appl 1
44	90.5	4.9	518	4	US-09-240-915-8	Sequence 8, Appl 1
45	90.5	4.9	518	4	US-09-591-435-8	Sequence 8, Appl 1

ALIGNMENTS

RESULT 1
PCT-US96-03916-7
Sequence 7, Application PC/TUS9603916
GENERAL INFORMATION:
Applicant: Cochran, Mark A.
Title of Invention: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
Title of Invention: AND USES THEREOF
Number of Sequences: 72
Correspondence Address:
Address: Cooper & Dunham LLP
Street: 1185 Avenue of the Americas
City: New York
State: New York
Country: U.S.A.
Zip: 10036
Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: Patent Release #1.25
Current Application Data:
Application Number: PCT/US96/03916
Filing Date: 23-MAR-1995
Classification:
Prior Application Data:
Application Number: US 08/126,597
Filing Date: 24-SEP-1993
Attorney/Agent Information:
Name: White, John P.
Registration Number: 28,678
Reference/Docket Number: 39116-A
Telecommunication Information:
Telefax: (212) 391-0525
Information for SEQ ID NO: 7:
Sequence Characteristics:
Length: 362 amino acids
Type: amino acid
Topology: linear
Molecule Type: protein
PCT-US96-03916-7
Query Match 100.0%: Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%: Pred. 2, 5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MASLIGTALLATLAPFGANGIYICNVASRIDDDHIVARPRATLOLFMPQ 60
1 MASLIGTALLATLAPFGANGIYICNVASRIDDDHIVARPRATLOLFMPQ 60

QY 61 RPKPKYSGTVAVAFRSIDTNOCYOESEERFENCNTHRSSVFNCKVETXFSASNLTG 120
DB 61 RPKPKYSGTVAVAFRSIDTNOCYOESEERFENCNTHRSSVFNCKVETXFSASNLTG 120
QY 121 PPHPKFTLNPNPNDSGMGYVIVRLDDTKEPIDVFAIQLSVQFANTATRLGLYSASC 180
DB 121 PPHPKFTLNPNPNDSGMGYVIVRLDDTKEPIDVFAIQLSVQFANTATRLGLYSASC 180
QY 181 RTGGLPTVOLEAVLRTREESRNNOAYVATEATTSAEATTPPTVATASASELAEHFTFP 240
DB 181 RTGGLPTVOLEAVLRTREESRNNOAYVATEATTSAEATTPPTVATASASELAEHFTFP 240
QY 241 WLENGVDHPEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
DB 241 WLENGVDHPEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
QY 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADDOSELVELVAIVNPALSPPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADDOSELVELVAIVNPALSPPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 2

PCT-US96-03916-68

Sequence 68, Application PC/TUS9603916

GENERAL INFORMATION:

APPLICANT: Wild, Martha A.

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/03916

FILING DATE: 23-MAR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/126,597

FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 39116-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO.: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 362 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-03916-68

Query Match 100.0%; Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLTALLAATLAFEGAMGIVITGNHVSANIDDDHIVIVAPREPAITQDLFFMPGQ 60
DB 1 MASLGLTALLAATLAFEGAMGIVITGNHVSANIDDDHIVIVAPREPAITQDLFFMPGQ 60
QY 61 RPKPKYSGTVAVAFRSIDTNOCYOESEERFENCNTHRSSVFNCKVETXFSASNLTG 120
DB 61 RPKPKYSGTVAVAFRSIDTNOCYOESEERFENCNTHRSSVFNCKVETXFSASNLTG 120
QY 121 PPHPKFTLNPNPNDSGMGYVIVRLDDTKEPIDVFAIQLSVQFANTATRLGLYSASC 180
DB 121 PPHPKFTLNPNPNDSGMGYVIVRLDDTKEPIDVFAIQLSVQFANTATRLGLYSASC 180
QY 181 RTGGLPTVOLEAVLRTREESRNNOAYVATEATTSAEATTPPTVATASASELAEHFTFP 240
DB 181 RTGGLPTVOLEAVLRTREESRNNOAYVATEATTSAEATTPPTVATASASELAEHFTFP 240
QY 241 WLENGVDHPEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
DB 241 WLENGVDHPEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
QY 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADDOSELVELVAIVNPALSPPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFPGPVACEINKGADDOSELVELVAIVNPALSPPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 3

US-08-709-731A-28

Sequence 28, Application US/08709731A

Patent No. 6322780

GENERAL INFORMATION:

APPLICANT: Lee, Lucy F.

APPLICANT: Nazerian, Keyvan

APPLICANT: Witter, Richard L.

APPLICANT: Wu, Ping

APPLICANT: Yanagida, No. 6322780oru

TITLE OF INVENTION: Marek's Disease Virus Genes and Their

TITLE OF INVENTION: Use in Vaccines for Protection Against Marek's Disease

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch and Birch, LLP

STREET: P.O. Box 747

CITY: Falls Church

STATE: VA

COUNTRY: US

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,731A

FILING DATE: 05-JUL-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/499,474

FILING DATE: 07-JULY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1644-110FPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO.: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE: internal
 ORGANISM: Marek's disease virus type I
 STRAIN: GA
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..355
 OTHER INFORMATION: /label= protein
 OTHER INFORMATION: /note= "91 protein"
 US-08-709-731A-28

Query Match 8.2%; Score 152; DB 4; Length 355;
 Best Local Similarity 22.9%; Pred. No. 1.2e-07;
 Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;

19 GAMGIYITGNHVSARIDDDHIVIVAPRPE-ATIQQLFEMPGQPHKPYSGIVAVAFRSD 77
 15 GIMSIYVYGTSTVLTSDQSALVAFGLDKMNVNRQQLFJDDOTRSTSTGTET-LKMD 73
 78 ITNOCYOEISEERENCNTHRSSVFVGCCKVTEYTFASNRLTGPHPFK--LITRNP 134
 74 EEKCYSLVHATSYMDCPADATVFRGCDAAVVAQPHDRV--QPEPEKGLRLIVEPRV 131
 135 NDSGMEYVIVRLDTPKEPIDVFAIQLSYQFANFAATRGILSKASCKTEGLPTVLEAVL 194
 132 SDTGSYIIFVALAG-RNMSDIFRMAVIRS-----SKSMACNHSASSFOAHKCI 179
 195 RTEE--SMENQAVYATETATTSATTPPTVATASASELAEHFTFPMLENGVDHYEPT 252
 180 RYVDRAAFENYLIQHVGLDSDSELHAIYINITPOSIS-TDINIITTFPDNSGTIYSP 238
 253 P--ANENSNVRLGT-MSPTLIGVVAAY--SATIGLIV--ISITRMCPHNRK 303
 239 VFMLFNHNVHDANSTGMNTVAKTLPELTYFSMLVLCIALIYLCERCRCRSPHRR 298
 304 LDTVSODDEESQTRRESRKRGPMVACEINKGADODSEIVE 344
 299 I-----YIGPRSD-----APLITSANVESPOVDYNYKE 328

RESULT 4
 US-08-344-833-2
 Sequence 2, Application US/08344833
 Patent No. 5874280
 GENERAL INFORMATION:
 APPLICANT: Kell, G. ether
 TITLE OF INVENTION: Recombinant Bovine Herpesvirus
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Organon Teknika Corporation
 STREET: 1330-A Piccard Drive
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,833
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Blackstone, William B.
 REGISTRATION NUMBER: 29,772
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 258-5200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-344-833-2

Query Match 7.9%; Score 148; DB 2; Length 317;
 Best Local Similarity 27.1%; Pred. No. 2.7e-07;
 Matches 68; Conservative 34; Mismatches 125; Indels 24; Gaps 11;

1 MASLGTALATLAFPGAMGIVITGNHVSARIDDDHIVIVAPREATIQ--OLFMP 58
 1 MRRLIMVVLAAABAP--ARSLVYRGEAVGIRADGPVAVRHP-ITDAILRGLTLE 57
 59 GGRP-HKPYSGTVAVAFRSDITNOCYOEISEERENCNTHRSSVFVGCCKVTEYTFASNR 117
 58 HQLPAGRRNGTVEL-LRYHAAGDCFVMLQTAFAFSCPRVANDAFRSCILADTRPARSER 116
 118 LGP--PHPEKLTIRNRPNDSCMFYIVRL---DTPKEIDVFAIQLSYQFAN--- 167
 117 RASAVENNVLEFSTARPRIDSGILFIRVGIYGTAGSERRRDVFPLAIVHSFGSPGD 176
 168 --TAATRGILYS--KASCRFTGLPTVQLVLEAYLTREESMNMQAVYATETTSATTP 223
 177 EAAAHPIGVVEARCRER-GLDASSASLYDALAAFPAGAA--TTPGPTASSSGAATP 233
 224 VTATSSELEA 234
 234 ERVDTEVEA 244

RESULT 5
 US-08-680-726A-56
 Sequence 56, Application US/08680726A
 Patent No. 5804197
 GENERAL INFORMATION:
 APPLICANT: Haanes, Elizabeth J.
 TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
 NUMBER OF SEQUENCES: 92
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/680,726A
 FILING DATE: 12-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-46-C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-680-726A-56

Query Match 7.9%; Score 148; DB 1; Length 364;
Best Local Similarity 27.3%; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

4 LGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATTQLOLFMPGQR-P 62
16 LLTTFPLIFLFLVNGVYKGTYSMLNTSSGFSIFPDDKFIYSGRLFLDDHLS 75
63 HKPYSGTVRAFRSDITNOCYQELSEERFENCTHRSSSVFVC--KVTEYTFASNRLTG 120
76 VNNVSGTIEFI--HFNNCTVYQTEIEYFSCPRIFNNAFSCCLKKYSKHHSQRLRINS 132
121 PPHPKLTINRPNDGSMFYIVRLDDTKEPIDVFAIQLSVQF 165
133 IENGVLLEITNPKPNDGSGVFIRVQLENK--TDVFGIPAFIYSF 175

RESULT 6
US-09-092-409-56
Sequence 56, Application US/09092409
Patent No. 6159478

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-092-409-56

Query Match 7.9%; Score 148; DB 4; Length 364;
Best Local Similarity 27.3%; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

4 LLGTLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATTQLOLFMPGQR-P 62
16 LLTTFPLIFLFLVNGVYKGTYSMLNTSSGFSIFPDDKFIYSGRLFLDDHLS 75
63 HKPYSGTVRAFRSDITNOCYQELSEERFENCTHRSSSVFVC--KVTEYTFASNRLTG 120
76 VNNVSGTIEFI--HFNNCTVYQTEIEYFSCPRIFNNAFSCCLKKYSKHHSQRLRINS 132

121 PPHPKLTINRPNDGSMFYIVRLDDTKEPIDVFAIQLSVQF 165
133 IENGVLLEITNPKPNDGSGVFIRVQLENK--TDVFGIPAFIYSF 175

RESULT 7

US-08-911-321-10
Sequence 10, Application US/08911321
Patent No. 6010703

GENERAL INFORMATION:

APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Foxvirus
TITLE OF INVENTION: Vaccine Against
TITLE OF INVENTION: Feline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
City: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096,183
FILING DATE: July 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 6010703e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 370
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Polypeptide
DESCRIPTION: Polypeptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: Deduced Sequence
OTHER INFORMATION: 91
US-08-911-321-10

Query Match 7.8%; Score 145; DB 3; Length 370;
Best Local Similarity 22.0%; Pred. No. 7.1e-07;
Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

5 LGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPRE-ATIQLOLFMPGQR-RP 62
1 MSIAFIYIIMAGITGVYGIYRDHVS LHVDTSGFVIYITLENFTLYGHLFLDDQRLP 60

RESULT 10
US-09-175-928-2
Sequence 2, Application US/09175928A
Patent No. 6312921
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racle, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: MI, Sha
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 387
TYPE: PRT
ORGANISM: Homo sapiens
US-09-175-928-2

Query Match
Best Local Similarity 19.2%; Pred. No. 0.0023;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

6.0%; Score 112; DB 4; Length 387;
Best Local Similarity 19.2%; Pred. No. 0.0023;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

1 MASLCTLALLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPATQQLFFMPGQ 60
12 LSLACQSVSVQYTI-PDGEVNTVGSNTLLICI---YTTVASRQLSTIOMSEFF----- 62
61 RPKPYSGYRVAFRSDITNQCQELSEERFENCSTRSSVFGSCVTEFTFSASRLTG 120
63 --HKKEPEPSTIF-----SOGGQVAIG-----OFKDRITG 92
121 PPHP--FKLIRNPRNDGSMFYIVRLDTPKEPIDVFAIQLSVYOFANTAATRGYSKA 178
93 SNDPGNASTISHMOPADSGIY-----ICDVNPPDFLQNGOGLNLSVLRP-----SKP 143
179 SCRTFLP---TVOLEAVIKRTESNRNMOAVATEATTTSATPTPTVATASLELA 224
144 LCSVQGRPEPTGHTISLSCL-----SALGTPSPV----- 171
235 EHTEFMLENGVDHYEPTPANENSNTV-----RLG----- 265
172 ----YTW--HKLEGRIVPKENFNPTTGLVIGNLNFEGGYOCTAINRLNLSCEID 225
266 -TWSPPLIGTVAAVYSAIIGLVISIVTRNNCTPHRLKLDTVSODDEERSQTRRESRKF 324
226 LTFSSHEVGIIVGALIGLGAIIISVY---CFARNKAKAKAK--ERNSKTIAE---L 276
325 GPMVACEINKGADODS---ELVELVAIVNPAL--SSPSIK 361
277 EPMT--KINPRGESEAMPREDATQLEVTLPSSIHETGPDTIQ 316

RESULT 11
US-08-190-802A-63
Sequence 63, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: P.O. Box 60850

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUPL, Fig. 46
US-08-190-802A-63

Query Match
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

5.8%; Score 108; DB 1; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

60 QRPKPYSGYRVAFRSDITNQCQELSEERFENCSTRSSVFGSCVTEFTFSASRLTG 115
86 QRDHQIASLTVLQD 144
116 NRTGPPHPFKLIRNPRNDGSMFYIVRLDTPKEPI-----D 154
145 NTTGSPSAF--PVQASRLVGS-----QLPTTLPVYSSNNQQLPQQLDQDQDQDQDQD 197
155 VFAIQLSVYOFANTAATRGYSKASCTRGFLPTVOL--EAVLRTESNRNMOAVY-----A 208
198 QPPQVSAVAPLSNTAING---SPTSKETTLPLPVKAPDESTLKETPEENNNTSKINDGSA 254
209 TEATTSAEAT--TPTPVATASLEAEHFTFPMLENGVDHYEPTP 253
255 TWTATTATETETKPEEDATPAS-LHODHYLVVYVNR-ANHSKPIP 295

RESULT 12
US-08-477-346-63
Sequence 63, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible


```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487, 072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: T0P1, Fig. 46
US-08-477-346-63

Query Match
5.8%; Score 108; DB 4; Length 713;
Best Local Similarity 27.3%; Pled. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11

QY 60 GRHKRYSGTYVAFRSDIINOCYGLSPRENCNTHRSSSVFGKTYEYFS----AS 115
DB 86 QRHQHSLSLTVQ000000000000Q0H0LQ0Q QQLAASASVYPAQPPATISATNPAA 144
QY 116 NRLTGPPHFKLTIRNRPNDSCMFYVIRLDTKERP-----D 154
DB 145 NRTTGPSPAF--PVQASFPNLVGS-----QLPTTLFPVSSNMQQLPQQLQ0QLOQ 197
QY 155 VFAIQLSVYQFNTAATRGILSKASCRTEGLPTVOL-FAIYRTDESRMKAIV-----A 208
DB 198 QPPQVSVAPLSNTAIN--SPTSKETTLLSVAPSPSTKETEPENNTISKINDTGA 254
QY 209 TEATTTSAEAT--TFPTVATASASELAEHFTFPWLENGVDHREPTP 253
DB 255 TTAATTTATETIKRKEDATPAP--LHODHYLVPNOR-ANHSKPIP 299

RESULT 13
US-08-473-089-63
; Sequence 63, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: The roof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC USA
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473, 089

```

```

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO.: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOG: unknown
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUP1, Fig. 46
US-08-473-089-63

Query Match          5.8%; Score 108; DB 4; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches, 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11.

OY   60 ORKHRYGATRVAFRRSDITNQCQCELSHERPENCSTRSSVYGCKYTEFFS---AS 115
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB   86 GRHQHSLATVQQQQQQQQQQQQQQQHLLQQQ-QQLAAASASVPVAQPPATSATAPPA 144

OY   116 NRTLGPHPFKLTIRNPDSGMFEVIVRLDDTKPEI-----D 154
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB   145 NTTSGPSNF--PVQASRPLVGS-----QLPTTLTVVSSNAQQQLPQQLQQQLQQ 197

OY   155 VFALISLYQQRANRAARGLXSASCRFGCLPYQL-EAYLFREESRMWQAIV----A 208
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB   198 QPPQVSVAPELNAINRG---SPTSKETTLPYSVAPESTLKETEEDENNNSKIINDGSA 254

OY   209 TEXTTTSAEAT--TPPYVTATNSLELAHFETFPMLEGDHYEPKP 253
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB   255 TTATTTATTEIKKEEDAIIPAS-LHQDHVLVPIYNQR-AHNSKRPIP 299

RESULT 14
US-08-487-072A-63
Sequence 63, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487, 072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

```


GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:09:18 ; Search time 15.5 Seconds
(without alignments)

2245.204 Million cell updates/sec

Title: US-09-993-777-7

Sequence: 1663 MASLGLTALLAATLAPPGA.....VELVAIVNPMSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	164	8.7	420	2 T42616	envelope protein -
2	162.5	8.7	354	1 VGBE67	glycoprotein D pre
3	153	8.3	353	1 C46113	glycoprotein D pre
4	153.5	8.2	424	1 VGBE63	glycoprotein gp63
5	143.5	7.7	350	1 VGBE63	glycoprotein gp63
6	140.5	7.5	380	2 S33785	glycoprotein I - b
7	125	6.7	356	2 J02352	glycoprotein I - t
8	124.5	6.7	356	2 T03146	probable glycoprot
9	115	6.2	457	1 RNMST4	cell surface gly
10	113.5	6.1	390	1 Q0BE77	glycoprotein I pre
11	111.5	6.0	149	2 A61162	glycoprotein I pre
12	108.5	5.8	355	2 C39725	hypothetical prote
13	108	5.8	713	2 JN0133	WD-40 repeat regul
14	107	5.7	372	1 Q0BE68	glycoprotein I pre
15	99	5.3	372	1 R3674	glycoprotein I pre
16	99	5.3	1036	2 S73601	glycoprotein I pre
17	98.5	5.3	1140	2 B3786	hypothetical prote
18	98	5.3	503	2 B38745	cell adhesion mole
19	98	5.3	507	2 S64507	probable membrane
20	97	5.2	1220	2 S493752	SN1 protein - yea
21	96.5	5.2	814	1 A39752	fibroblast growth
22	95.5	5.1	797	1 VGBE61	glycoprotein X pre
23	95.5	5.1	867	2 T45463	membrane glycoprot
24	95	5.0	1777	2 T34369	hypothetical prote
25	94	5.0	796	2 T21460	hypothetical prote
26	93.5	5.0	645	2 T29818	hypothetical prote
27	93.5	5.0	907	1 Q0BE21	membrane antigen g
28	93.5	5.0	3020	2 A43932	mucin 2 precursor,
29	93	5.0	1051	2 S55259	TfPI protein - mou

30	92.5	5.0	1778	2 AF1116	internalin protein
31	92	4.8	1044	2 P05375	probable drug resi
32	91.5	4.8	510	2 T47374	hypothetical prote
33	91	4.8	365	2 A34424	Cod4 membrane gly
34	90.5	4.8	836	2 S49940	cell division cont
35	90.5	4.9	577	1 S28904	intercellular adhe
36	90.5	4.9	785	2 T37329	probable oligopept
37	90.5	4.9	786	2 T19017	hypothetical prote
38	90.5	4.9	1429	2 T41699	C2-domain family p
39	90	4.8	233	2 C84193	hypothetical prote
40	90	4.8	798	2 T34248	hypothetical prote
41	89.5	4.8	826	2 G90283	hypothetical prote
42	89.5	4.8	866	2 T45462	membrane glycoprot
43	89.5	4.8	929	2 T38817	hypothetical prote
44	89	4.8	692	2 AE1525	probable peptidog
45	89	4.8	678	2 S54308	DNA binding protei

ALIGNMENTS

RESULT 1

T42616
envelope protein - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42616
R:RefSeq: E. A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J:Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: Z22173; MUID:98264497; PMID:9603335
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T42616
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-420 <REP>
A:Cross-references: EMBL:AF030027; MUID:92605950; PIDN:ACG59593.1; PID:92606021
A:Experimental source: strain NS80567
C:Genetics:
A:Note: 73
C:Superfamily: pseudorabies virus glycoprotein gp63

Query Match 8.8%; Score 164; DB 2; Length 420;

Best Local Similarity 25.5%; Pred. No. 9.6e-06; Mismatches 143; Indels 88; Caps 21;

Matches	96	Conservative	50	Mismatches	143	Indels	88	Caps	21
OY	10	LLAATLAPGAMGIVTGNHVSARIDDDHIVAPPEATLQ-LFFMGOQ-PKPKPS	67						
DB	13	LIAISMCM--ATAIYRGHMSMTLINSSEFAVYPRKSLVVGMLFDGQRLPTTNS	69						
OY	68	GTVAFAFRSDITWOCYOEISEREENCTHRSSVFGC--KVETYESASRLTGPPHP	125						
DB	70	GLIEL-IHNHYSHGCVSYIOTISYSCPRVANNAFRSCLAKTSNHNODYFHVNTSVETNV	128						
OY	126	KLTFRNRPDPMGFVYIRLDLDTKEPIDVFAIQLSVQF-ANTATRGLYSKASCRTEG	184						
DB	129	LLNTRPOPADSGAYILRVKLHNA-PRADYFGSAFVYDQNSNTPVEPPTAKPSPNVET	187						
OY	165	LPTVOLFAVYRTESWRNMOAVATEATTSAAET--TPPTVTASASELAEHFTFP	241						
DB	188	RTAPAPAPANSTK-----TGSNNTSSOSTWMLYPTP-----RPA	221						
OY	242	LENGVDYDEPTPANEN--SNVTVR-----GTMSPP-----LIGVVAVVSATIG	285						
DB	222	LEF---HLLTAPANEVVSAGDTAMLCHEFRSTAVPTIYHLLGLT-----GMPE	269						
OY	286	--LVIVSIVTRMKCPHKKLDTS-----ODDERSGOTREER-KFGPMV-----ACEIN	333						
DB	270	DVLELDESELR---TPPKPOTISSRTGDDFGQNTSPSKRNKIYAMVVIPTACVL	326						
OY	334	KGADDSLEYELVAIYN 350							
DB	327	-----LLLVVGAIIIN 337							

RESULT 2

VGBE67

glycoprotein D precursor - human herpesvirus 3

N:Alternate names: glycoprotein IV

C:Species: human herpesvirus 3, varicella-zoster virus

C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999

C:Accession: F27345

R:Davidson, A.J.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A:Title: The complete DNA sequence of varicella-zoster virus.

A:Reference number: A27345; MUID:86306657; PMID:3018124

A:Accession: F27345

A:Molecule type: DNA

A:Residues: 1-354 <DAV>

A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27950.1; PID:g60056

C:Gene: g6

C:Superfamily: herpesvirus glycoprotein D

Keywords: glycoprotein; phosphoprotein; transmembrane protein

-17/Domain: signal sequence #status predicted <SIG>

F:279-295/Domain: transmembrane #status predicted <GPD>

F:33,47,67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted:

Query Match 8.7%; Score 162.5; DB 1; Length 354;
 Best Local Similarity 22.4%; Pred. No. 1e-05;
 Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

QY 23 IVTGNHVSARIDDDHIVAPPRE--ATIQLEFPMQORP-HKPYSGTVARFSDI 78
 DB 21 LIRKGVHVSQVNSLSLILIPQNDNYTEIKQLVFIGQLPTGTVSGTLELLY-ADR 79
 79 TNCYOELSEERENCNHRSSVFGCKV--EYFESASNRLTGPHPRKLTIRNRPN 135
 DB 80 VACFHSVQVIRIDGCPRIATSAFISCRVYKSHMHTGNDRISTEPAGWMLITPKGIN 139
 QY 136 DSGMFYVIRLDDTKEPIDVFIQLSVY-----QFANTAATGLYSKAS 179
 DB 140 DACVYVYVLRDLHSRS-TDGFILGVNVYTAGSHHNGVITYTSPSLONGYSTALFQQA- 197
 QY 180 CRFFGLPT-----VQLEAVLRTEES-WRMQAVVATEATTATTAETTPRPV 225
 DB 198 -RACDLPAPPKSGSTLFOHMLDLRAGKSLSDNPMLH-EDVVTETKRSVYKEG----- 248
 QY 226 ATASELEAEHFTFPMLENCVDHYEPTPAN---ENS-----NVTYVRLGTMSPTLIGTV 276
 DB 249 -----IEN---HYVPTDKSTLPEKSLNDPEMLLI-----IIPIVA 281
 DB 277 AAVVSATIGLIVISIVTRNM 297
 DB 282 SVMILTAMVIVIVISVKKRRI 302

RESULT 3

C46113

glycoprotein D precursor - cercopithecine herpesvirus 9 (strain DHV)

N:Alternate names: membrane glycoprotein 1

C:Species: cercopithecine herpesvirus 9

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: C46113

R:Fletcher III, T.M.; Gray, W.L.

Virol. 193, 762-773, 1993

A:Title: DNA sequence and genetic organization of the unique short (Us) region of the st

A:Accession: C46113

A:Molecule type: DNA

A:Residues: 1-353 <FLE>

A:Cross-references: GB:L07067; NID:g310715; PIDN:AAA47888.1; PID:g310718

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-353/Product: glycoprotein D #status predicted <GPD>
 F:275-293/Domain: transmembrane #status predicted <TMN>
 F:40,75,84,122,138,227,252/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 8.3%; Score 155; DB 1; Length 353;
 Best Local Similarity 20.2%; Pred. No. 4.2e-05;
 Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY 18 FG---AMGIVITGNHVSARIDDD--HIVAPPREATIQLEFPMQORP-HKPYSGTV 71
 DB 20 FGIOCAAIIRNYISLYVNSSATSIIFLGKNNNDASIRRFLEIGQFPVTNTYNTVE 79
 QY 72 VAFRSIDTNCYOELSEERENCNHRSSVFGCKV--EYFESASNRLTGPHPRKLTIR 130
 DB 80 L-LHVNOTTLCLOPLXVVMGECPRITGALICRVRSWHYENAOQLDPNVEIIFKMN 138
 QY 131 NRPNDSCMFYVIRLDDTKEPIDVFIQLSVYQFANTAATRGLYSASRTGGLPYOL 190
 DB 139 NTVVEDAGIYLLVQLDYT-SLFDIFPVSLNVPKQDTSMEDVY-----FPEVYS 188
 QY 191 EAV-LRTEESMRMQAVVATEATTSAETTPRPVATSAELEAEHFTFPMLENCVDHY 249
 DB 189 PSHILNFKIKCHFPYHNGMSGILCHIV-----SDVDTERENLSMKDLDGST 238
 QY 250 EPPANENSNTVYRL-----GTMSPTLIGTVAAVVSATIGLIVISI-VTRNMC 298
 DB 239 QKPRKNFNPDKVNVTHETKRTLMSSADVEMIAVPTASLVLAILIIVTVGIYRRRS 298
 QY 299 TPRKIDTVSODDEERSQTRRE 320
 DB 299 SEKRKYPRKTRKQASTERRE 320

RESULT 4

VGBE9

glycoprotein gp63 precursor - equine herpesvirus 1

N:Alternate names: glycoprotein I precursor; hypothetical 46k protein; ORF2 protein

C:Species: equine herpesvirus 1

A:Note: host Equus caballus (domestic horse)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: C36646; J00998; A36803

R:Audonnet, J.C.; Winslow, J.; Allen, G.; Paoletti, E.

J. Gen. Virol. 71, 2969-2978, 1990

A:Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with h

A:Reference number: A36646; MUID:91108393; PMID:2177089

A:Accession: C36646

A:Molecule type: DNA

A:Residues: 1-424 <NDU>

A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Kentucky D

R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.

Gene 101, 203-208, 1991

A:Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesvir

A:Reference number: J00998; MUID:91276272; PMID:1647559

A:Accession: J00998

A:Molecule type: DNA

A:Residues: 1-424 <ELT>

A:Cross-references: GB:M36299; NID:g330787; PIDN:AAA6547.1; PID:g330788

R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

submitted to GenBank, March 1992

A:Description: The DNA sequence of equine herpesvirus-1.

A:Reference number: A36803

A:Accession: A36803

A:Molecule type: DNA

A:Residues: 1-424 <TEL>

A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Ab4p

R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

Virol. 189, 304-316, 1992

A:Title: The DNA sequence of equine herpesvirus-1.

A:Reference number: A41831; MUID:92295566; PMID:1318606

A:Contents: annotation; possible protein-coding frames

A:Note: neither amino acid nor nucleotide sequence is given

[illegible]

THIS PAGE BLANK (USPTO)


```

CC      or send an email to license@slsb.sib.ch)
CC
DR      EMBL; L07067; AAA47888.1;  -
DR      PIR; C46113; C46113.
DR      InterPro; IPR002874; Herpes_g1.
DR      Pfam; PF01688; Herpes_g1; 1.
DR      Glycoprotein; Transmembrane; Signal.
FT      SIGNAL      1      20
FT      CHAIN      21      353
FT      DOMAIN      21      274
FT      TRANSMEM      275      293
FT      DOMAIN      294      353
FT      CARBOHYD      40      40
FT      CARBOHYD      75      75
FT      CARBOHYD      84      84
FT      CARBOHYD      122      122
FT      CARBOHYD      138      138
FT      CARBOHYD      227      227
FT      CARBOHYD      252      252
SO      SEQUENCE      353 AA; 40470 MW; E0314F7B5B04AA2 CRC64;

Query Match      8.3%; Score 155; DB 1; Length 353;
Best Local Similarity 20.2%; Pred. 0.1.le-05;
Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY      18 FG---AMGIVTGNHVSARIDDD-HIYVAPREATQLOLFEMPGRP-HKPYSGTVR 71
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      20 FGIOCAALIIYRGVNIISLYVNSSATSIPLKNNNDASIRGRFLFGDOPVTNTNTVAVE 79

QY      72 VAFSDITNOCYQELSEERFENCJHRSSVFGCV-TEYFSA SNRLTGPHPKLTIR 130
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      80 L-LHVNOTTLLDPLRYRWYGECPRIKRGATLACVKKSMHYENATQLLDPVETIEFKMN 138

QY      131 NRPNDSGMFYVYIALDQTEPIDVFAIQLSVGYOFANATRGLYSKASCTFSLPTVOL 190
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      139 NTKVEDAGIILLYVQLODT-SLFDLFFSLVNYPRQDTSNDVNV-----PPPYYS 188

QY      191 EAV-LRTEESNRNMOAYVATEATTSAEATPTPYATASASELEAENHFFPLENGVDHY 249
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      189 PSHLNTFFKICKHPFVNHGMEOSILOHIVT-----SDVPTETENLSMOKDLCST 238

QY      250 EPTPANENSNTVNR-----GIMSPLIGITVAANYASATIGLIVYISI-VTRMMC 298
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      239 QKPRKNFPDVKVNVHTETKRTLMESSADVEMIAVPITASLVLITLIVTVGIGRRRS 298

QY      299 TPHRKLDVTSODDEERSQTRRE 320
           || : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      299 SEKKRIYRKRRTKQASTEKRE 320

RESULT 3
VGLI_HSVEB      STANDARD;      PRT;      424 AA.
ID      VGLI_HSVEB
AC      P18553;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Glycoprotein I precursor.
GN      GI OR 73.
OS      Equine herpesvirus type 1 (strain Ab4p) (EHV-1),
OS      Equine herpesvirus type 1 (strain ABI) (EHV-1), and
OS      Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OS      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Alphaherpesvirinae; Varicellovirus.
OC      NCBI_TaxID=31520, 10328, 10330;
OX
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AB4p;
RX      MEDLINE=92295566; PubMed=1318606;
RA      Telford E.A.R., Watson M.S., McBride K., Davidson A.J.;
RT      "The DNA sequence of equine herpesvirus-1.";
RL      Virology 189:304-316(1992).
LN      [2]
LN

```

RP SEQUENCE FROM N.A.
 RC STRAIN-AB1;
 RA MEDLINE-91276272; PubMed-1647359;
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;
 RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
 RT herpesvirus type-1 short unique region."
 RT Gene 101:203-208(1991).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-Kentucky D;
 RA MEDLINE-9108333; PubMed-2177089;
 RA Audonnet J.-C., Hunslow J., Allen G., Paolletti E.;
 RT Equine herpesvirus type 1 unique short fragment encodes
 RT glycoproteins with homology to herpes simplex virus type 1 gp, g1 and
 RT g2.
 RT J. Gen. Virol. 71:2969-2978(1990).
 RL J. Gen. Virol. 71:2969-2978(1990).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
 CC AND TO PRV GP63.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M86664; AAC02508.1; -
 CC DR EMBL: M36299; AAA6547.1; -
 CC DR PIR: C36646; VGBEE9.
 CC DR PIR: J00998; J00998.
 CC DR PIR: A36803; VGBEG4.
 CC DR InterPro: IPR002874; Herpes-g1.
 CC DR Pfam: PF01688; Herpes-g1; 1.
 CC DR Glycoprotein: Signal; Transmembrane.
 CC KW SIGNAL 1 22
 CC FT CHAIN 23 424
 CC FT DOMAIN 23 319
 CC FT TRANSMEM 320 340
 CC FT DOMAIN 341 424
 CC FT CARBOHYD 35 35
 CC FT CARBOHYD 67 67
 CC FT CARBOHYD 78 78
 CC FT CARBOHYD 121 121
 CC FT CARBOHYD 131 131
 CC FT CARBOHYD 236 236
 CC FT CARBOHYD 307 307
 CC SEQUENCE 424 AA; 46392 MW; EEB9EF7DA895806 CRC64;
 CC -----
 CC Query Match 8.28; Score 153.5; DB 1; Length 424;
 CC Best Local Similarity 23.88; Pred. No. 1; 9e-05; Indels 57; Gaps 12;
 CC Matches 70; Conservative 41; Mismatches 126;
 OY 1 MASLLGTLAALTAAPGANGIVITGNHVSARIDDDHIVYAPREPTIOL-QLFPMG 59
 DB 1 MAKLTGMSAAILLSMAICSAITLIRGEHMSMTLNSSEFAYFPDQSLVGLHFLD 60
 OY 60 QR-PHKRYSGTVAFRSDITNOCYQELSEEFENCNTHRSSVFGC-KYTEYTSASN 116
 DB 61 ORLPPTNYSGLIEL-IHNYVSVCTVYQITISYSCPRVANAFAFSCIAKTSKHYADYR 119
 OY 117 RUTGPRHPFKLTIRNRPNDGSMFYIVRLDQTEKPIDVFAIOLSVYQFANTATRG 176
 DB 120 VNASVETNVLINIKKPOIPDSGAYILRVKIDHA-PTADVFQVSAFVYL 167
 OY 177 KASCRTEGLPTVO---LEAYLRTEESMRMNOAVVATEATTS---AAATTPPVATSA 229
 DB 168 KSKVYPMWPTTQTVPEPTTSYSTPTDYDTDEETESTISTOOAMTSTQTP-SATWG 226
 OY 230 SELEAHEHTPMLNGVDHTEPTPANENSNTVRLG-----TMSPTL 271

DB 227 TQLTTE-----LPTNE---TVVIGQALLCHWQDPSTREPTL 260
 RESULT 4
 ID VGLI_PVRI STANDARD; PRT; 350 AA.
 AC P07646
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glycoprotein GP63 precursor.
 OS Pseudorabies virus (strain Rice) (PRV).
 OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 NC NCBI TaxID=10350;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE-86308235; PubMed-3018284;
 RA Petrovskis E.A., Timmins J.G., Post L.E.;
 RT "Use of lambda g11 to isolate genes for two pseudorabies virus
 RT glycoproteins with homology to herpes simplex virus and varicella-
 RT zoster virus glycoproteins."
 RT J. Virol. 60:185-193(1986).
 RL J. Virol. 60:185-193(1986).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, AND TO VZV
 CC GP1V.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M14336; AAC35204.1; -
 CC DR PIR: A29012; VGBE63.
 CC DR InterPro: IPR002874; Herpes-g1.
 CC DR Pfam: PF01688; Herpes-g1; 1.
 CC DR Glycoprotein: Transmembrane; Signal.
 CC KW SIGNAL 1 23
 CC FT CHAIN 24 350
 CC FT DOMAIN 24 285
 CC FT TRANSMEM 286 308
 CC FT DOMAIN 309 350
 CC FT CARBOHYD 56 56
 CC FT CARBOHYD 73 73
 CC FT CARBOHYD 153 153
 CC FT CARBOHYD 226 226
 CC FT CARBOHYD 262 262
 CC FT CARBOHYD 275 275
 CC SEQUENCE 350 AA; 36773 MW; 66AF2229EC21BEDA CRC64;
 CC -----
 CC Query Match 7.78; Score 143.5; DB 1; Length 350;
 CC Best Local Similarity 22.88; Pred. No. 0.00011; Indels 87; Gaps 17;
 CC Matches 82; Conservative 42; Mismatches 149;
 OY 8 LALLAATLAPFGAM--GIVITGNHVSARIDDDHIVYAPREPTIOLQLFPMGCRPHKP 65
 DB 15 LLLAALLTALTPRVGVLFRGAGSVNVAAGSAVLPGDAPVLITDGLFLFGPSPS- 73
 OY 66 YSGTVAFRSDITNOCYQELSEEFENCNTHRSSVFGC-KYTEYTSASN---NL 118
 DB 74 YSGRVEL-LRLDPRKACTRYEAAEYDLICRVHNEFRCCCKRPLARRASAAVAPAR 132
 OY 119 TGRPHRPFKLTIRNRPNDGSMFYIVRLDQTEKPIDVFAIOLSVYQFANTATRG 174
 DB 123 ---LFSRNPAPDAGSVYLRVNGT---TDLFVLTALV-----PRGRPHHP 174
 OY 175 -YSKASCRTEGLPTVOLEAYLRTEESMRMNOAVVATEATTS---AAATTPPV 224
 DB 175 TPSSADCR---PV-----GSHDSLRYVDPAADAVFTTPPIEPEPTTPAP 221

QY 225 TATSAS-----ELEHEFTPEWLENGVDHYEPANENSNTVRLGWSPTLIGVTA 277
 DB 222 RGTGATPEPESDEEED-----EGATPAMPPEPTLDTANGTM---VYNASVSVLL 271
 QY 278 AVVSATG-----LVIVSYTRMNCPTPHKRLDVSODDERSGOTRRRSRK 323
 DB 272 AANAATGANGPCKIAMVLTPTVLTFLUGVACARRCARGIASTGRGARRSTR 331

RESULT 5

VGLI_HSVBS STANDARD: PRT: 380 AA.
 ID VGLI_HSVBS
 AC 008102;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glycoprotein I.
 GN GI.
 OS Bovine herpesvirus type 1.2 (strain ST).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Alphaherpesvirinae; Varicelloviruses.
 NCBI_TaxID=45407;
 [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-94167875; PubMed-8122370;
 RA Leung-Trick P., Audonnet J.F., Riviere M.;
 RT "The complete DNA sequence and the genetic organization of the short
 RT unique region (US) of the bovine herpesvirus type 1 (ST strain).";
 RL Virology 199:409-421(1994).
 CC -1- SIMILARITY: NO OTHER HERPESVIRUSES GLYCOPROTEIN I, TO VZV GP1V,
 AND TO PRV GP63.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).

DR EMBL: 223068; CA80605.1;
 DR InterPro: IPR002874; Herpes_g1.
 DR Pfam: PF01688; Herpes_g1.
 KW Glycoprotein.

FT CARBOHYD 67
 SQ SEQUENCE 380 AA: 39910 MW: AEBELFB9B430D2BD CRC64: (POTENTIAL).

Query Match 7.5%; Score 140.5; DB 1: Length 380;
 Best local similarity 25.3%; Pred. No. 0.0002;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;

QY 1 MASLLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPATIQ--OLEFMP.58
 DB 1 MRCLLLMVYLARAP--ARSLYRGEAVGLRADGPVAFVAP--TDTATLALGRILFLE 57
 QY 59 GQRP-HKPSGTRVAFRSITNOCYOELSEEFENCNHRSSSVFPGCKTETTFASNR 117
 DB 58 HQPACRRNGVEL-LRYHAAGDCFVMTQTFAFCPRVANAARFSCCLADRRPARSER 116
 QY 118 LTPP--PHPEFKLTIRNPDPDSGMFYIVRL---DDTKEPIDVPAIQLSVYQFA----- 166
 DB 117 RASAVENHVLFEIARPRIDSLYFLRNGITYGCTAGSEKRRROVFPPLAAVHSGFGEGDP 176
 QY 167 -----NTAATRGILYSASCRTEGL-----PTVQLEAVLRTEESWR 201
 DB 177 EAAARTPARSGRSPASGITSASLYDRALANSPOAPPRAAPRAAARGPRRPERVDE 236
 QY 202 NMOAVATEATTTSACATPTPTATASAS 230
 DB 237 TTEEAATRAGSAFALTTPAGTASPAA 265

RESULT 6

CD4_MOUSE
 ID CD4_MOUSE STANDARD: PRT: 457 AA.
 AC P06332;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
 DE T4/Leu-3) (T-cell differentiation antigen L3T4).
 GN CD4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87018845; PubMed-3094146;
 RA Tourville B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;
 RT "Isolation and sequence of L3T4 complementary DNA clones: expression
 RT in T cells and brain.";
 RL Science 234:610-614(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87115821; PubMed-3027575;
 RA Littman D.R., Gettner S.N.;
 RT "Unusual intron in the immunoglobulin domain of the newly isolated
 RT murine CD4 (L3T4) gene.";
 RL Nature 325:453-455(1987).
 [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-brain;
 RX MEDLINE-88152875; PubMed-3326818;
 RA Parnes J.R., Hunkapiller T.;
 RT "L3T4 and the immunoglobulin gene superfamily: new relationships
 RT between the immune system and the nervous system.";
 RL Immunol. Rev. 100:109-127(1987).
 [4]
 RP SEQUENCE FROM N.A. (BRAIN FORM).
 RC TISSUE-brain;
 RX MEDLINE-88041159; PubMed-2823269;
 RA Gorman S.D., Tourville B., Parnes J.R.;
 RT "Structure of the mouse gene encoding CD4 and an unusual transcript
 RT in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98112780; PubMed-9445485;
 RA Ansari-Pari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RT "Comparative sequence analysis of a gene-rich cluster at human
 RT chromosome 12p13 and its syntenic region in mouse chromosome 6.";
 RL Genome Res. 8:29-40(1998).
 [6]
 RP SEQUENCE OF 27-43.
 RX MEDLINE-86166694; PubMed-3082751;
 RA Claesson B.J., Tsagaratos J., Kirsbaum L., Maddox J., McKay C.R.,
 RA Brandon M., McKenzie I.F.C., Walker I.D.;
 RT "The L3T4 antigen in mouse and the sheep equivalent are
 RT immunoglobulin-like.";
 RL Immunogenetics 23:129-132(1986).
 [7]
 RP DISULFIDE BONDS.
 RX MEDLINE-86233454; PubMed-3086886;
 RA Claesson B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
 RT "Partial primary structure of the T4 antigens of mouse and sheep:
 RT assignment of intrachain disulfide bonds.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
 CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
 CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
 CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M36850: AAA39401.1; -
 CC EMBL: M13816: AAA37267.1; -
 CC EMBL: X04836: CAA28539.1; -
 CC EMBL: M36851: AAA39402.1; -
 CC EMBL: M17080: AAA37403.1; -
 CC EMBL: M17078: AAA37403.1; JOINED.
 CC EMBL: M17079: AAA37403.1; JOINED.
 CC EMBL: AC002397: AAC36010.1; -
 CC PIR: A02110: RNMST4.
 CC PIR: A26038: A26038.
 CC HSSP: P01730: IWR.
 CC MOD: MGI:88335; Ccd4.
 CC InterPro: IPR000973; CD4_TCA.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003600; Ig_Like.
 CC InterPro: IPR003596; Ig_V.
 CC Pfam: PF00047; Ig_1.
 CC PRINTS: PR00692; CD4TCANTIGEN.
 CC SMART: SM00410; Ig_Like; 2.
 CC SMART: SM00406; IgV_1.
 CC Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
 CC Immune response; Repeat; Signal; Lipoprotein; Palmitate;
 CC Alternative splicing.
 CC
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 457
 CC FT DOMAIN 27 457
 CC FT TRANSSEM 395 417
 CC FT DOMAIN 418 457
 CC FT DOMAIN 418 457
 CC FT DOMAIN 128 128
 CC FT DOMAIN 129 207
 CC FT DOMAIN 208 317
 CC FT DOMAIN 318 374
 CC FT CARBOHYD 187 367
 CC FT CARBOHYD 296 358
 CC FT CARBOHYD 323 353
 CC FT CARBOHYD 323 353
 CC FT DISULFID 152 188
 CC FT DISULFID 328 370
 CC FT DISULFID 418 418
 CC FT LIPID 421 421
 CC FT ASPARTIC 1 240
 CC SEQUENCE 457 AA: 51296 MW: 181DA7527CB00F33 CRC64;
 CC
 CC Query Match 6.2%; Score 115; DB 1; Length 457;
 CC Best Local Similarity 20.6%; Pred. No. 0.035;
 CC Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;
 CC
 CC 19 GAMGIVITGNHVSARIIDDDHIVAPREPTIOLDF--FMGGRPHKPYSGTVRAFR 75
 CC 93 GSFPLIT--NLIKMEQSQTYICELNRE--EVELWFKYFSGSLGSLTLTLDN 149
 CC 76 SDITNOCYOELSEERFENCNTHSSSVFCKYVETYSNRLTGPFPFKLITRPNRP 135
 CC 150 SKVSN---PLTE---CKHKRGKVGSGSKV-----LSMSNLRVQ 181
 CC 136 DSGMYVIVIRLDDTKPEIDVFAIOLSVYQFANTATAGLYSKASCFTGLPTVLEAYLR 195
 CC 182 DSDFNCTVTLDOKK--NMFGWTLISVLGFOSTAIT--AVYSBESAESFPLNRAE--- 233
 CC 196 TEBSNRN--WQAVYVTEATYTSSEATPTPTVATASSELAEHFTFPLNENGVHDEPT 253
 CC 234 -ENGWGEIMWKA-----KDSFQPMISFINKKEYSV 265

CC 254 ANENSVVTRIGTMSPTLIGVAVVSAITGLIVISIVTRNCKTPHRLTYSODDEE 313
 CC 266 QKSTKQIKQIKLKEPLTLKIPVSLQFAGSGLN---TLTLDKGLHDEVNLYWKAQ 321
 CC 314 RSOTRRESKPPPMVACEIN-----KGAQD--SELVELVAIVNPSA----- 353
 CC 322 LNTN-----LTCEVMGPTSPKMLTLKQENDEARVSEDEKVVQVAVPETGLMOCL 371
 CC 354 LSPDSTIKM 362
 CC 372 LSEGDYKM 380
 CC
 CC RESULT 7
 CC ID VGLI_HSV11 STANDARD; PRT; 390 AA.
 CC AC P06487;
 CC DT 01-JAN-1988 (Rel. 06, Created)
 CC DT 01-JAN-1988 (Rel. 06, Last sequence update)
 CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
 CC DE Glycoprotein I.
 CC GN GI OR US7.
 CC OS Herpes simplex virus (type 1 / strain 17).
 CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC NCBI_TaxID=10299;
 CC RX MEDLINE=85160822; PubMed=2984429;
 CC RA McGeeoch D.J., Dolan A., Donald S., Rixon F.J.;
 CC "Sequence determination and genetic content of the short unique
 CC region in the genome of herpes simplex virus type 1".
 CC J. Mol. Biol. 181:1-13(1985).
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GE, AND GF.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUS GLYCOPROTEINS I, TO VZV GIV,
 CC AND TO PRV GP63.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: L00036: AAA06681.1; -
 CC EMBL: X41116: CAA32284.1; -
 CC EMBL: X02438: CAA26061.1; -
 CC PIR: A05243: OCBE77; Herpes-GI.
 CC InterPro: IPR002874; Herpes-GI.
 CC Pfam: PF01688; Herpes-GI; 1.
 CC Glycoprotein I.
 CC CARBOHYD 156 156
 CC CARBOHYD 175 175
 CC CARBOHYD 257 257
 CC SEQUENCE 390 AA: 41369 MW: 39381B1D655F0808 CRC64;
 CC
 CC Query Match 6.1%; Score 113.5; DB 1; Length 390;
 CC Best Local Similarity 20.8%; Pred. No. 0.038;
 CC Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;
 CC
 CC 7 TLTAATLAPFGAMGIVITGNHVSARIIDDDHIVAPREPTIOLDF--FMGGRPHK- 65
 CC 27 TVSLVSNSEFVADALD-----PDGVVEEDLLID-----ELREYGVQVPHIT 69
 CC 66 YSGTVRAVAFSDITNOCYOELSEERFENCNTHSSSVFCKYVETYSNRLTGPFP 125
 CC 70 YDGVDEL-WHYRPMGHGCRPVHVVYVATACPRRPAVAFALCRATIDSTHS-----PAYET 121
 CC 126 -----KLITRNPDPDSCMEYVIVIRLDDTKPEIDVFAIOLSVYQFANTATAGLYS 176

OS Herpes simplex virus (type 2 / strain 333).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10313;
RN [1]
RP MEDLINE=86291145; PubMed=3016980;
RX Hodgman T.C., Minson A.C.;
RA "The herpes simplex virus type 2 equivalent of the herpes simplex
RT virus type 1 US7 gene and its flanking sequences."
RT Virology 153:1-11(1986).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEIN IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M14886; AAA45861.1; -
CC EMBL: D00026; BA00021.1; -
CC PIR: A05246; Q08588.
CC InterPro: IPR002874; Herpes_g1.
CC Pfam: PF01688; Herpes_g1; 1.
CC
CC Glycoprotein.
CC CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 372 AA: 39548 MW: 83942 DD:20D8ADBD CRC64;
SO
Query Match 5.78; Score 107; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.12; 163; Indels 64; Gaps 13;
Matches 74; Conservative 51; Mismatches 163;
OY 3 SLGCTALLAATLAPFGAMGIVTGNVSRIDDDHIVYAPREAIOL-----QLFF 56
DB 5 SLOG-LALIGLWVC---ATGLVNGPTVSL-VSDSLVDAGAVGPGFVEDDLAVFGLHF 59
OY 57 MGGORPKPKYSGTVAVARSDITNOCQOESEERFENCNHRSSVFGCKVTEYTSASN 116
DB 60 VGAOVPHNTNYDGIIELEHPLGNHCRVHVVTTLACRRRAVAFTLCSTHANS--- 116
OY 117 RLUGPRHPF-----KLITRNPRNDGSMFYVYRLDD-TKEPIDVFIOLSYOFA 166
DB 117 ---PAVPTLELGLAROPILNRATRDYAGLYLVWVGATNSRLVGLVALS---A 168
OY 167 NTAATRGLYSKASCRFTGLPTVOLEAVLRTEESRMWQVYVATEATTTSAAATTPPVTA 226
DB 169 NGTFVNGSYGSCDPAQLP-----FSAPRLGPSVYTPASPAPPPPT 212
OY 227 TSASELEAEHFTPEMLENGVDHYEPTPANENSNVYRLGTMSPPTLIGTVAAVVSATIGL 286
DB 213 TTSPSSPRDPTPAFG-----DTGTPAPASGEIAPPNSTASSESHRRLTVAOYIOAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRESKRGKGP-MVACEINKGA 336
DB 268 SLIAFVFLGSCICFIHRC-----QRRYRRPRGQIYNPGVSCAVNEA 310
RESULT 10
VGLI_HSV2H STANDARD: PRT; 372 AA.
AC P13291;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glycoprotein I.

GN GI OR US7.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10313;
RN [1]
RP MEDLINE=87111457; PubMed=3027242;
RX Mcecech D.J., Moss H.W.M., McNab D., Frame M.C.;
RA DNA sequence and genetic content of the HindIII 1 region in the
RT DNA sequence component of the herpes simplex virus type 2 genome;
RT Identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons." J. Gen. Virol. 68:19-38(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DDAJ databases.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X04798; CA28485.1; -
CC EMBL: Z86099; CAB06714.1; -
CC PIR: F43674; F43674.
CC InterPro: IPR002874; Herpes_g1.
CC Pfam: PF01688; Herpes_g1; 1.
CC
CC Glycoprotein.
CC CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 372 AA: 39558 MW: 83958 DD:20D8ADBD CRC64;
SO
Query Match 5.38; Score 99; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.38; 165; Indels 64; Gaps 13;
Matches 74; Conservative 49; Mismatches 165;
OY 3 SLGCTALLAATLAPFGAMGIVTGNVSRIDDDHIVYAPREAIOL-----QLFF 56
DB 5 SLOG-LALIGLWVC---ATGLVNGPTVSL-VSDSLVDAGAVGPGFVEDDLAVFGLHF 59
OY 57 MGGORPKPKYSGTVAVARSDITNOCQOESEERFENCNHRSSVFGCKVTEYTSASN 116
DB 60 VGAOVPHNTNYDGIIELEHPLGNHCRVHVVTTLACRRRAVAFTLCSTHANS--- 116
OY 117 RLUGPRHPF-----KLITRNPRNDGSMFYVYRLDD-TKEPIDVFIOLSYOFA 166
DB 117 ---PAVPTLELGLAROPILNRATRDYAGLYLVWVGATNSRLVGLVALS---A 168
OY 167 NTAATRGLYSKASCRFTGLPTVOLEAVLRTEESRMWQVYVATEATTTSAAATTPPVTA 226
DB 169 NGTFVNGSYGSCDPAQLP-----FSAPRLGPSVYTPASPAPPPPT 212
OY 227 TSASELEAEHFTPEMLENGVDHYEPTPANENSNVYRLGTMSPPTLIGTVAAVVSATIGL 286
DB 213 TTSPSSPRDPTPAFG-----DTGTPAPASGEIAPPNSTASSESHRRLTVAOYIOAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRESKRGKGP-MVACEINKGA 336
DB 268 SLIAFVFLGSCICFIHRC-----QRRYRRPRGQIYNPGVSCAVNEA 310
RESULT 11

P200_MYCPN STANDARD: PRT; 1036 AA.
ID P200_MYCPN
AC P75211; Q50346;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein P200.
GN P200 OR MPN567 OR MP275.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxId=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=96257197; PubMed=8675035;
RA Profit T., Hilbert H., Plagens H., Herrmann R.;
RT "The P200 protein of Mycoplasma pneumoniae shows common features with
RT the cytochrome-associated proteins HmM1 and HmM3.";
RL Gene 171:79-82(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
RN [3]
RP SEQUENCE OF 641-678 FROM N.A.
RC STRAIN-ATCC 29342 / M129; PubMed=7984111;
RX MEDLINE=95075318; PubMed=7984111;
RA Profit T., Herrmann R.;
RT "Identification and characterization of hitherto unknown Mycoplasma
RT pneumoniae proteins.";
RL Mol. Microbiol. 13:337-348(1994).
CC -1- FUNCTION: PROTEIN CYTOSKELETON-ASSOCIATED WHICH COULD BE AN
CC ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U25989; AAC99815.1; -
CC EMBL: AE000027; AAB95923.1; -
CC EMBL: Z52646; CA83569.1; -
CC Cytadherence; Structural protein; Repeat; Complete proteome.
FT DOMAIN 277 280 POLY-THR.
FT DOMAIN 300 845 PRO-RICH.
FT DOMAIN 357 360 POLY-THR.
FT DOMAIN 401 404 POLY-ALA.
FT DOMAIN 718 781 3 X 6 AA REPEAT OF E-P-E-P-N-F.
FT REPEAT 718 723 1.
FT REPEAT 738 743 2.
FT REPEAT 776 781 3.
FT REPEAT 776 781 3.
FT CONFLICT 641 641 A -> P (IN REF. 3).
SQ SEQUENCE 1036 AA; 116915 MW; DESAEABAB6DD95B29 CRC64;
Query Match 5.3%; Score 99; DB 1; Length 1036;
Best Local Similarity 23.9%; Pred. No. 2.2;
Matches 57; Conservative 29; Mismatches 90; Indels 62; Gaps 10;
QY 127 LTRNRPRDSCMFYIVRLDTPKEPIDVFAIQLSYQFAN--TAATRGVLSKASCRFP 183
DB 446 VVIDNQPOAGFHYVDFLTST-APLTYAELELODELNEFVTTSTRRTTFFASTPVF 504
QY 184 G--LPTVLEAVLTREESMRNQAVVATEATTSADATP--TPVATSASELEAEH 236
DB 505 EPVIVTFVSEBQLENE-----FVESTVVSATSNPEPNASTPVEVET----- 546

QY 237 FTEPWLGVHDYEPPEPANENSVTVRLGTMSPFLIGVY-----AAVVSATIGL 286
DB 547 -----VELTE-TPVSLPELETYQLVETAPVTEVTVTEKAVEPEVLAVVEAPLAV 596
QY 287 VYIYSTVRMKCTPHRKLDTVSODDEBSOTRESKRF--PVACEINKAGQDSSEL 342
DB 597 EPVETST-----TLAAETVEAOVEBESVAVAVEAETESKATSEAOEL 643
RESULT 12
YD76_MYCPN STANDARD: PRT; 1140 AA.
ID YD76_MYCPN
AC P75405;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN376 (A19_071140).
GN MPN376 OR MP460.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxId=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN375.
CC
CC -1- SIMILARITY: IN THE CENTRAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN374.
CC
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN373.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE000045; AAB96108.1; -
CC EMBL: A0000045; AAB96108.1; -
CC Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 1098 1118 POTENTIAL.
SQ SEQUENCE 1140 AA; 130383 MW; 8FA9406C57DD8886 CRC64;
Query Match 5.3%; Score 98.5; DB 1; Length 1140;
Best Local Similarity 20.5%; Pred. No. 2.7; Indels 91; Gaps 15;
Matches 68; Conservative 53; Mismatches 119;
QY 71 RVAFRSIDITNOC-YQELSERERE-NCTHRSSSVFVCGKTEYTFSSNRLTGPFPFKLT 128
DB 680 RERFQKIDNNYLKVGQISERIKVNAVHVDAALNKRKSDPLAS--VQSTANKYGLN 736
QY 129 IR-NPRPNDSCMFYIVY-----RLDDTK-----EPIDVFAIQLSYQFAN-- 167
DB 737 LRSNPY--TGQFYVVDVDTNANDLGNORRANKAKSYFYIEGLDKGAQSSYLVRPENO 793
QY 168 -----TAATRGVLSKASCRFPGLPTVQLEAVLTREES-----WRNQAVVATEATT 213
DB 794 KLYSLESLAVDSKGLYK-----NWSKDIIDAKONULYLDTHMNA--ALKALU 842
QY 214 TSAEATTPPVVATSASELEAEHFEPTPWLGVHDYEPPEPANENSVTVRLGTMSPFLIG 273
DB 843 TNAELTLPT-ASADNSAKLS-----TPNENDE-----GLSLSNVSG 878
QY 274 VYVAAVVSATIGLVYIYSTVRNM-----CTPHRKLDTVSODDEBSOTRRE 320

0y	321	SRKPGPVACINKGADQDSEIVEVAIVNP	351	
Db	939	AKGVNVLVSEKGDDESDKNIFKITLTNP	969	
RESULT 13				
ID	CD44_RAT	STANDARD:	PRT:	503 AA.
AC	126051:	0990021:		
DT	01-NOV-1992	(Rel. 22, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	CD44 antigen precursor (Phagocyte glycoprotein I) (Pgp-1) (Hunch-1)			
DE	(Extracellular matrix receptor-III) (ECM-III) (Sp9 lymphocyte			
DE	homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)			
DE	(1y-24).			
DE	CD44.			
DE	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
OX	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	STRAIN-BDIX: TISSUE=Pancreas;			
RX	MEDLINE-91191552; Pubmed-107342;			
RX	Genther U., Hofmann M., Rudy W., Reber S., Zoeller M.,			
RA	Hausmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.,			
RT	"A new variant of glycoprotein CD44 confers metastatic potential to			
RT	rat carcinoma cells."			
RL	Cell 65:13-24(1991).			
RP	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1).			
RA	Stevens J.W., Midura R.J.;			
RA	Submitted (Jan-1996) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: MAIN CELL SURFACE RECEPTOR FOR HYALURONATE. ADHESION TO			
CC	MUCOSAL HIGH ENDOTHELIAL VENULE AND TO TYPES I AND VI COLLAGEN.			
CC	PROBABLY INVOLVED IN MATRIX ADHESION, LYMPHOCYTE ACTIVATION AND			
CC	LYMPH NODE HOMING.			
CC	-1- SUPRACELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: At least 2 isoforms: 1/short form and 2/long			
CC	form/meta-1 (shown here); are produced by alternative splicing.			
CC	-1- PTM: EXTENSIVELY MODIFIED INCLUDING N- AND O-LINKED GLYCOSYLATION,			
CC	ADDITION OF THE GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, OF SULFATE,			
CC	OF PHOSPHATE TO CYTOPLASMIC DOMAIN SERINE RESIDUES.			
CC	-1- SIMILARITY: CONTAINS 1 LINK DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation at			
CC	the European Bioinformatics Institute. There are no restrictions on any			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: M61875; AAA53532.1; -			
CC	EMBL: M61874; AAA53534.1; -			
CC	EMBL: U52179; AAA97915.1; -			
CC	EMBL: U46957; AAA92920.1; -			
CC	HSSP: P98066; ITSC.			
DR	InterPro: IPR001231; CD44 antigen.			
DR	InterPro: IPR000538; Link.			
DR	pfam: PF00193; xlink: 1.			
DR	PRINTS: PR00658; CD44.			
DR	ProDom: PD000918; Link: 1.			
DR	SMART: SMD0445; Link: 1.			
DR	PROSITE: PS01241; Link: 1.			
KW	Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation;			
KW	Receptor; Proteoglycan; Sulfation; Signal; Alternative splicing.			
FT	SIGNAL	1	21	
FT	CHAIN	22	503	CD44 ANTIGEN.

[illegible]

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: 272974; CAA97215.1; -
 DR EMBL: X99074; CAA67525.1; -
 DR HSP: P23904; IAKK.
 DR SGD: S0003421; CRH1.
 DR InterPro: IPR000757; Glyco_hydro_16.
 DR Pfam: PF00722; Glyco_hydro_16; 1.
 KW Hypothetical protein.
 FT DOMAIN 63 66 POLY-SER.
 FT DOMAIN 301 310 POLY-SER.
 FT DOMAIN 345 357 POLY-SER.
 FT DOMAIN 387 391 POLY-SER.
 FT DOMAIN 467 470 POLY-SER.
 SO SEQUENCE 507 AA; 52757 MW; 7D7B61F57AE942C CRC64;

Query Match 5.3%; Score 98; DB 1; Length 507;
 Best Local Similarity 21.7%; Pred. No. 1.1;
 Matches 54; Conservative 46; Mismatches 95; Indels 54; Gaps 9;

136 DSGMFVIRLDPTKPIDVFAIQLSVQFANTATRGYSKASCRFGLPVQLEAYLR 195
 278 DGGSIY--GRYDQAGDFAVLANGSSSTSSSTSVSSASSTSVSSASST 335
 196 TEBSWNRMOAYVATEATTSAEATPTPTVATNSASELEAHFTFPLENGVDHYEPTPAN 255
 336 VSSS---VSTVSSSSSSSSSTSPSSSTATSSKTLASSVT---TSSSISFE-KOSS 388
 256 ENSNVTVRIGTMTPTLIGT-VAAYVSATIGLVISITRNKCTPHRKLDITYSOD---- 310
 389 SSSKRTVASSSTSESTISSTKTPATVSSVST-----TRSTVAPPTQSSVSSDSPVQ 438
 311 -----DEERSQTRRESRKFGPMV-----ACEINKGADOD-----S 340
 439 DKGAVATSSNDVTSSTQTSSKRTSTIQSSSSASSSTNSVQISNGADLQSLPREKLTFS 498
 341 ELVELVAIV 349
 499 VLVALALL 507

RESULT 15
 ID SLN1_YEAST STANDARD; PRT; 1220 AA.
 AC P39928;
 DT 01-FEB-1995 (Rel. 31, Created)
 RT 01-FEB-1995 (Rel. 31, Last sequence update)
 GN 15-JUN-2002 (Rel. 41, Last annotation update)
 OS Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
 GN SLN1 OR YP02 OR YIL147C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae;
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / YPH1;
 RX MEDLINE=94024010; PubMed=8211183;
 RA Ota I.M., Varshavsky A.;
 RT "A yeast protein similar to bacterial two-component regulators";
 RL Science 262:566-569(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Genes S., Hamlyn N., Horneill T.S., Hunt S., Jagsels K., Jones M.,
 RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles S., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.

[3]
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE=94239498; PubMed=8183345;
 RA Maeda T., Wurgler-Murphy S.M., Salto H.;
 RT "A two-component system that regulates an osmosensing MAP kinase
 cascade in yeast";
 RL Nature 369:242-245(1994).
 CC - FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
 CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK2->
 CC PROTEIN->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
 CC STIMULATE THE PBS2-HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
 CC THE ACTIVATED SLN1 HISTIDINE KINASE REPRESENTS THE ACTIVATION OF THE
 CC PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
 CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC - PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
 CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
 CC DOMAIN.
 CC - SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC - SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL: Z38059; CAA6131.1; -
 DR EMBL: 001835; AAC48912.1; -
 DR PIR: S48888; S48888.
 DR HSP: P06143; IUDR.
 DR SGD: S0001409; SLN1.
 DR InterPro: IPR003594; ATPbind_Atpase.
 DR InterPro: IPR004358; Bact_sens_ptc.
 DR InterPro: IPR004359; His_Kin_sig.
 DR InterPro: IPR003661; His_KinA.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; response_reg. 1.
 DR Pfam: PF00512; signal. 1.
 DR Pfam: PF02518; HATPase_c. 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR ProDom: PD000039; Response_reg. 1.
 DR SMART: SM00387; HATPase_c. 1.
 DR SMART: SM00388; HSKA. 1.
 DR SMART: SM00448; REC. 1.
 DR PROSITE: PS50109; His_Kin. 1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY. 1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 POTENTIAL.
 FT DOMAIN 47 333 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 334 354 POTENTIAL.
 FT DOMAIN 355 1220 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 573 928 HISTIDINE KINASE.
 FT DOMAIN 1089 1210 RESPONSE REGULATORY.
 FT MOD_RES 576 576 PHOSPHORYLATION (AUTO-) (PROBABLE).
 FT MOD_RES 1144 1144 PHOSPHORYLATION (PROBABLE).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 576 576 H->Q: INACTIVE.
 FT MUTAGEN 891 891 G->D: SLOW GROWTH, SLN1-1 MUTANT.
 FT MUTAGEN 1144 1144 D->N: INACTIVE.
 SO SEQUENCE 1220 AA; 134434 MW; 45FEE24A8165468B CRC64;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:08:23 ; Search time 28 Seconds

(without alignments)
2663.895 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863

Sequence: 1 MASLIGTALLAATLAPFGA.....VELVAIVNSALSSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VIRTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	12	Q67645 gallid herp
2	164	8.8	420	12	Q39309 equine herp
3	162.5	8.7	354	12	Q38VNI human herp
4	158	8.5	420	12	Q35325 equine herp
5	156	8.4	384	12	Q69357 feline herp
6	154	8.3	384	12	Q66931 feline herp
7	152	8.2	355	12	Q69615 turkey herp
8	149	8.0	355	12	Q69287 turkey herp
9	148	7.9	364	12	Q9YPA1 canine herp
10	148	7.9	364	12	Q41525 canine herp
11	147	7.9	259	12	Q91335 canine herp
12	145	7.8	370	12	Q86789 feline herp
13	140.5	7.5	369	12	Q91E39 phocid herp
14	139.5	7.5	382	12	Q39505 bovine herp
15	130.5	7.0	366	12	Q99F67 pseudorabid
16	125	6.7	356	12	Q88524 turkey herp

17	124.5	6.7	683	12	Q36401 alcelaphine
18	123	6.6	355	12	Q67638 gallid herp
19	115	6.2	433	11	Q55054 mus musculu
20	115	6.2	457	11	Q61396 mus musculu
21	108.5	5.8	319	5	Q9M357 drosophila
22	106.5	5.7	235	12	Q9DY19 bovine herp
23	103	5.5	982	5	Q9VIG1 drosophila
24	102.5	5.5	378	4	Q96H15 homo sapien
25	102.5	5.5	4498	5	Q9M223 drosophila
26	99	5.3	279	5	Q9U474 caenorhabdi
27	99	5.3	1011	5	Q9NH29 heliooverpa
28	97.5	5.2	1714	5	Q9M1X4 drosophila
29	96.5	5.2	814	13	Q91897 xenopus lae
30	96	5.2	877	4	Q9H306 homo sapien
31	96	5.2	878	4	Q9H307 homo sapien
32	96	5.2	957	4	Q9H307 homo sapien
33	96	5.2	1217	4	Q9UKW9 homo sapien
34	95.5	5.1	332	12	Q8VOM9 equine herp
35	95.5	5.1	337	12	Q8VOM1 equine herp
36	95.5	5.1	342	12	Q8VOM8 equine herp
37	95.5	5.1	356	12	Q8VOM7 equine herp
38	95.5	5.1	357	12	Q8VOM2 equine herp
39	95.5	5.1	372	12	Q8VOM3 equine herp
40	95.5	5.1	374	12	Q8VOM6 equine herp
41	95.5	5.1	389	12	Q8VOM0 equine herp
42	95.5	5.1	826	12	Q8VOM5 equine herp
43	95.5	5.1	867	12	Q39782 equine herp
44	95	5.1	745	5	Q9VYU8 drosophila
45	95	5.1	1844	5	Q22579 caenorhabdi

ALIGNMENTS

RESULT 1	ID	Q67645	PRELIMINARY:	PRT:	362 AA.
AC	Q67645				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	Glycoprotein 1.				
OS	Gallid herpesvirus 1.				
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.				
OX	NCBI_TaxID=10386;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-USDA CHALLENGE STRAIN;				
RX	MEDLINE=9703380; PubMed=8879127;				
RA	Wald M.A., Cook S., Cochran M.;				
RT	"A genomic map of infectious laryngotracheitis virus and the sequence				
RT	and organization of genes present in the unique short and flanking				
RT	regions.";				
RL	Values Genes 12:107-116(1996).				
DR	EMBL: U28832; AAC55101.1; -				
DR	InterPro: IPR002874; Herpes_g1.				
DR	Protein: PF01688; Herpes_g1; 1.				
SO	SEQUENCE 362 AA; 59750 MW; F530CIAFTCCGBAS CMC64;				
QY	Query Match	100.08;	Score 1863;	DB 12;	Length 362;
QY	Best Local Similarity	100.08;	Pred. No. 1.3e-160;	Indels	0;
QY	Matches 362;	Conservative	0;	Mismatches	0;
QY	1	MASLIGTALLAATLAPFGANGIVITGNHVSARIDDDHIVIAVPAPEATIQLOLEFEPQ	60		
QY	1	MASLIGTALLAATLAPFGANGIVITGNHVSARIDDDHIVIAVPAPEATIQLOLEFEPQ	60		
QY	61	RPHPKPSGVVRAAFRSDITNOCYOELSEEFENCSTRSSSVFGCKVETTFSSANRLTG	120		
QY	61	RPHPKPSGVVRAAFRSDITNOCYOELSEEFENCSTRSSSVFGCKVETTFSSANRLTG	120		
QY	61	RPHPKPSGVVRAAFRSDITNOCYOELSEEFENCSTRSSSVFGCKVETTFSSANRLTG	120		
QY	121	PPHPFKLIRNRPNDSCMFYIVRLDTPKEPIDVPAIOLSVYQAPNTAATRGVYSKASC	180		

```
Db 121 PPHFKLITRNPRNDGSMFYVLRDITKEPIDVFAIQLSVQFAMTAIRGLYSKASC 180
Qy 181 RTGCLPTVQLEAVLRTEESRNMQAVYATATTSABATTPTPTATTSASELEAHEHTFP 240
Db 181 RTGCLPTVQLEAVLRTEESRNMQAVYATATTSABATTPTPTATTSASELEAHEHTFP 240
Qy 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVIVISIVTRNMCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVIVISIVTRNMCTP 300
Qy 301 HRKLDIVYQDDEERSQTRRSRKGPMVACEINKGADQDSEIVEIVAVNPSALSSPDSI 360
Db 301 HRKLDIVYQDDEERSQTRRSRKGPMVACEINKGADQDSEIVEIVAVNPSALSSPDSI 360
Qy 361 KM 362
Db 361 KM 362
```

RESULT 2

```
039309 PRELIMINARY; PRT; 420 AA.
AC 039309;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Counterpart of HSV-1 gene US7 and VZV gene 67.
GN 73.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=10331;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed-9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4."
RL J. Gen. Virol. 79:1197-1203(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RL Submitted (OCT-1997) to the EMBL/Genbank/DBU databases.
DR EMBL: AF030027; AAC59593.1;
DR InterPro: IPR002874; Herpes-g1.
DR Pfam: PF01688; Herpes-g1; 1.
SQ SEQUENCE 420 AA; 45710 MW; 1EB944825DF3D852 CRC64;
```

Query Match 8.8%; Score 164; DB 12; Length 420;
Best Local Similarity 25.5%; Pred. No. 1.8e-06;
Matches 96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;

```
Qy 10 LAAATLAPGAMGIVTGNHVSARIDDDHIVYAPREAIQQLFFMGQR-PHKRYS 67
Db 13 LLAISMCC--ATAIIRGEHMSMYLNASSEFAVYPRKDSLVVGHMLFDGQLPTTNS 69
Qy 68 GTVAVAFRSDITNOCYOELSEERFENCOTHRSSVFVGC--KTEYTFASNRLTGPHP 125
Db 70 GLEEL-IHNHNSGCGSVIQTISYESCPRVANNAFRSCLHKTSNNHODTFHVVTSETVN 128
Qy 126 KLTIRNPRNDGSMFYVLRDITKEPIDVFAIQLSVQFAMTAIRGLYSKASCRTFG 184
Db 129 LNTIRFPQADSGAYILRLKLNHA-PTADVFGSAFVYDLOSNVTPEVPYAKEPSNVFT 187
Qy 185 LPTVQLEAVLRTEESRNMQAVYATATTSABATTPTPTATTSASELEAHEHTFP 241
Db 188 RPPAPAPATSTK-----TGSNTTSSOSTLWYPTP-----RPA 221
Qy 242 LENGVDHYEPTPANEN--SNVTVRL-----GTMSPT-----LIGVTAAVVSATIG-- 285
Db 222 LET---HLTTAANETVYSGDTAMLCGFRPSTIAVPTIYMHILGLT-----GNLPE 269
```

```
Qy 286 --IVIVISIVTRNMCTPHRKLDIVS-----QDDEERSQTRRSR-KRPMV---ACEIN 333
Db 270 DVLLIEDSEILR---TPPRKQPTTSSRTBEDDFKQNTSTSPKSNKIVAAVVIPTACVLM 326
Qy 334 KGADQDSEIVEIVAVN 350
Db 327 -----LLVVGAIIN 337
```

RESULT 3

```
098VN1 PRELIMINARY; PRT; 354 AA.
AC 098VN1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE ORF67.
OS Human herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=10335;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RX MEDLINE=21109116; PubMed-11162813;
RA Faga B., Maury W., Bruckner D.A., Grose C.;
RT "Identification and Mapping of Single Nucleotide Polymorphisms in the Varicella-zoster Virus Genome."
RL Virology 280:1-6(2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RA Cole N.L., Faga B.P., Grose C.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DBU databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-VIA;
RA Grose C., Faga B.;
RT "Identification and mapping of single nucleotide polymorphisms in the Varicella-zoster virus genome."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBU databases.
DR EMBL: AF314221; AKK19249.1;
DR EMBL: AF325441; AAK01055.1;
DR InterPro: IPR002874; Herpes-g1.
DR Pfam: PF01688; Herpes-g1; 1.
SQ SEQUENCE 354 AA; 39373 MW; 3F01739F3AFC6B08 CRC64;
```

Query Match 8.7%; Score 162.5; DB 12; Length 354;
Best Local Similarity 22.4%; Pred. No. 2e-06;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

```
Qy 23 IVITGNHVSARIDDDHIVYAPRE--ATIQQLFFMGQR-PHKRYSQVAVAFRSDI 78
Db 21 LIRKGDHVSILQVNSSLTSLIPQNDNYETIKQLVFIGQLGTGNYSGTLELL-ADT 79
Qy 79 TNOCYOELSEERFENCOTHRSSVFVGCKYT---EYTFASNRLTGPHPFKLITRNPRN 135
Db 80 VAFCEFSVQVIRDGCPRIRTSAFISCRKHSNHYGNSIDRISTEDDAGVMLKITRPGIN 139
Qy 136 DSGMFYVIRLDITKEPIDVFAIQLSVQFAMTAIRGLYSKAS 179
Db 140 DAGVYVLRDLHSRS-TDGFILGVVYVAGSHNHIGVITYTSPSLONGYSTRALFQA- 197
Qy 180 CRTFGIPT-----VQLEAVLRTEES-WRMQAVYATATTSABATTPTPT 225
Db 198 -RUCDIPATPKSGTSLFQHMIDLRLRAGKSLDNPMLH-EDVVTTERKSVYKKG----- 248
Qy 226 ATSASELEAHEHTFPMLENGVDHYEPTPAN-----NVYRLGTMSPTLIGVTV 276
Db 249 -----IEN---HYVPTDMSITLPEKSLNDPENLLI-----IIPYIA 281
Qy 277 AAVVSATIGLVIVISIVTRNM 297
```



```

SQ SEQUENCE 384 AA; 43019 MW; C9ACEL429E496DC1 CRC64;

Query Match 8.3%; Score 154; DB 12; Length 384;
Best Local Similarity 22.3%; Pred. No. 1.3e-05;
Matches 73; Conservative 52; Mismatches 133; Indels 70; Gaps 13

OY 5 LCTLLAATLTPFGAMGAVITGNHVSATIDDDHIYVAPRE-ATIQQLFPMGQ-RP 62
DB 1 MSSTAFITLMAIGVYIGVGRGDHVSLSHVDTSSGVVITPLENTIYCHLFLDDPRLP 60
OY 63 HKPQGVAVAFRSDITNOCYQELSEERENCNTHRSSVAVGC-KVTEYTSASNRLTG 120
DB 61 VANNNGTLEI-IHYNHSSCYKIVQYIEYSSCPVRNNAFRCGLKHTSMHQDQLSINIS 119
OY 121 PPHPKLTIARNRPDSCGFYIVIRLDDIKEPDLVFAIDLSYQFANTATRGYSKASC 180
DB 120 VETGMILLITTSFKMEDGCIYALRVRFNNHK-ADVEGLSVFYVSF---DTRGRHHADE 174
OY 181 RTFGV--LPTVQ-LEAVLRTFESRMNQAV---VATEATTSAEATPTPVATASASELDA 234
DB 175 NLNGELITTPSPMEYIVKV-----NTPYIDHVVITQTTSNKSNSEPSNTSISC----- 223
OY 235 EHFTPEWLENGVDYEPFPANENSNTVRL-----GTMSPLTIGTVAA 278
DB 224 -----HFFQNDPNEGELTYHLNLINAGNITVDWMQGTLLKPRIDGNLNL 270
OY 279 VVSAT-----IGLYIYISI 292
DB 271 SVTSSFKNETTOKMTPDRKVGFIYISI 298

RESULT 7
OY 09E6L5 PRELIMINARY; PRT; 355 AA.
AC 09E6L5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE US7 membrane glycoprotein I-like protein.
GN MDY095.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10390;
RX [1]
RC SEQUENCE FROM N.A.
RP STRAIN-MDS.
RX MEDLINE=20392152; PubMed=10933706;
RX Tutman E.R., Alfonso C.L., Lu Z., Zsak L., Kutish G.F.;
RX "The genome of a very virulent Marek's disease virus."
RX J. Virol. 74:7980-7988(2000).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-MDS;
RC Tutman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF243438; AAC14269.1;
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI: 1_gI.
SQ SEQUENCE 355 AA; 40568 MW; D23A6DA126ACDB00 CRC64;

Query Match 8.2%; Score 152; DB 12; Length 355;
Best Local Similarity 22.9%; Pred. No. 1.8e-05;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14

OY 19 GAMGVITGNHVSATIDDDHIYVAPRE-ATIQQLFPMGQRPKPSGTVAVAFRSD 77
DB 15 GIMSVIVYGTSTLSTFSDSALVAFGGLDKMNVVRQQLFLGDQTRTSYTGTEI-LKMD 73
OY 78 ITNOCYQELSEERENCNTHRSSVAVGC-KVTEYTSASNRLTGPPHPK---LTIARNPP 134
DB 74 EYKCYSTVLHATSYMDCAIDATVYRGCGRDAVYVAQPHDRV--QFPPEKGLIRLIVEPRV 131

```

QY	133	NSGMEFYVYRLDDKPEFLDVAIQLSVQFANTATRLRYKASCRTEGCLPQVQLEATL	194
DB	132	ISGTSYIRFVALAG-RNMSDIFPMALVIRS-----SKSMACNHSASSFOAHKCI	179
QY	195	PREE--SWRMQOAVYATEATTTSAAETPTPTATASASELEAHEFTFPMLENGVDHDEPT	252
DB	180	KYVDNMAEFNYLIGHVGNLDDSDSELHAIYNITPOIS-TDINIITTPPYDINSGITTSPT	238
QY	253	P--ANENSNTVRLGT-MSPTLIGVTVAAV--SATIGLVIV--ISIVTRNCTPHRK	303
DB	239	VENLENNNSHVDAMNSTGMNTVLKTTPLRLIYFSMTIVLCIALAIYVCECRNSPHRR	298
QY	304	LDTVSODDEERSQTRRESKRFQPMVACEINRKADDSOLVE	344
DB	299	I---YIGEPRSDE-----APLITSAVNESFOYDYNKE	328
RESULT 8			
ID	069287	PRELIMINARY:	PRT: 355 AA.
AC	069287;		
DT	01-NOV-1996 (TREMblrel. 01, Created)		
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)		
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)		
DE	Membrane glycoprotein 1 precursor.		
GN	US7.		
OS	Turkey herpesvirus.		
CC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Marek's disease-like viruses.		
OX	NCBI_TaxId=10390;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95133166; PubMed=7831788;		
RA	Brunovskis P., Velicer L.F.;		
RT	"The Marek's disease virus (MDV) unique short region:		
RT	alphaherpesvirus homologous, fowlpox virus homologous, and MDV-		
RT	specific genes."		
RL	Virology 2016:324-338(1995).		
DR	EMBL; L22174; AAA64968.1;		
DR	InterPro: IPR002874; Herpes_g1.		
-DR	Pfam: PF01688; Herpes_g1.1.		
KW	Signal.		
FT	SIGNAL 1 18	POTENTIAL.	
FT	CHAIN 19 355	MEMBRANE GLYCOPROTEIN 1.	
SO	SEQUENCE 355 AA; 40579 MW; 40CD25034E4EAE6F CRC64;		
Query Match 8.0%; Score 149; DB 12; Length 355;			
Best Local Similarity 23.3%; Pred. No. 3.3e-05;			
Matches 80; Conservative 54; Mismatches 163; Indels 46; Gaps 15			
QY	19	GAMGIVITGNHNSARIDDDHIVAPR--PEATIQQLFPMGPGRPHKPSGYVAVAR	75
DB	15	GIMSIYVIGTSTV-LSTDQSALVAFRGDKKVVNVRGQLFLGDQTRTSYGTETI-LK	71
QY	76	SDITMOQOELSEEPKENTHRSSSVFYGCCKATETTFSSANLITGPAPHFK--LTIRNP	132
DB	72	WDEEKYCSVLTATSYMCPADATAVFRCRCRAVYVAOPHGV--QPFPEKGTLLRIYEP	129
QY	133	RNDGSMGFVYIRLDDTEKPIDVPAIQLSVQFAMTAATRGVSKASCRTEGCLPQVQLEA	192
DB	130	RVSDDGYIIRYSLAG-RMSDIFPMVVIIRS-----SKSMACNHSASSFOAHK	177
QY	193	YLRTEE--SWRMQOAVYATEATTTSAAETPTPTATASASELEAHEFTFPMLENGVDHDE	250
DB	178	CIRYVDNMAEFNYLIGHVGNLDDSDSELHAIYNITPOIS-TDINIITTPPYDINSGITTS	236
QY	251	PTP--ANENSNTVRLGT-MSPTLIGVTVAAV--SATIGLVIV--ISIVTRNCTPH	301
DB	237	PTVENLFINNSHVDAMNSTGMNTVLKTTPLRLIYFSMTIVLCIALAIYVCECRNSPH	296
QY	302	RKLDTVSODDEERSQTRRESKRFQPMVACEINRKADDSOLVE	344
DB	297	RRI---YIGEPRSDE-----APLITSAVNESFOYDYNKE	328

```

RESULT 9
O9YPAL ID O9YPAL PRELIMINARY: PRT: 364 AA.
AC O9YPAL:
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Similar to HSV-1 gI.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSL-2;
RA MEDLINE=98185505; PubMed=9524817;
RA Tyack S.G., Studdert M.J., Johnson M.A.;
RA "Nucleotide sequence of canine herpesvirus homologues of herpes
RT simplex virus type 1 US2, US3, glycoproteins I and E, US8.5 and US9
RT genes."
RL DNA Seq. 7:365-368(1997).
DR EMBL: U49380; AAC67213.1;
DR InterPro: IPR002874; Herpes_gI.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF01688; Herpes_gI.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 364 AA: 41999 MW; B9BC33EE7FB913A9 CRC64;

Query Match 7.9%; Score 148; DB 12; Length 364;
Best Local Similarity 27.3%; Pred. No. 4.2e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGVITGNHVSARIDDDHIVAPRPAATIQQLFFMPGQR-P-62
DB 16 LITMFLPTLFLFYGNGFYKGYISMFLNTSSGFSIFPDOKFVSGRLFLDDQHLS 75
OY 63 HKPYSGTVAVAFRSDITNOCYQELSEBERENCTHRSSVFGC--KVETTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYQTIEFSCPRIFNNAFSCCLKVKSHESQLRINS 132
OY 121 PPHPEKLTIRNRPNDSCGFYIVRLDDTKREPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKRNDSCGFYIVRQLENNK--TDVFGIPAFIYSF 175

ULT 10
525
O41525 PRELIMINARY: PRT: 364 AA.
AC O41525:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CUS7 (glycoprotein I).
GN GI.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RA Haanes E.O., Tomlinson C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-YPI1M0;
RA MEDLINE=98455388; PubMed=9784067;
RA Nishikawa Y., Xuan X., Otsuka H.;
RT "Identification and characterization of the glycoprotein E and I genes
RT of canine herpesvirus."
RL Virus Res. 56:77-92(1998).
RN [3]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-AUSTRALIAN;
RA Reubel G.H., Pekin J., Webb-Wagg K., Hardy C.M.;
RT "Nucleotide sequence of glycoprotein genes B, D, G, H and I, thymidine
RT kinase and protein kinase genes and gene homologue UL 24 of an
RT Australian isolate of canine herpesvirus."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U84223; AB67059.1;
DR EMBL: AB003728; BAA33765.1;
DR EMBL: AF361076; BAA31063.1;
DR InterPro: IPR002874; Herpes_gI.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF01688; Herpes_gI.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 364 AA: 42068 MW; 08BC32E7FB913A8 CRC64;

Query Match 7.9%; Score 148; DB 12; Length 364;
Best Local Similarity 27.3%; Pred. No. 4.2e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGVITGNHVSARIDDDHIVAPRPAATIQQLFFMPGQR-P-62
DB 16 LITMFLPTLFLFYGNGFYKGYISMFLNTSSGFSIFPDOKFVSGRLFLDDQHLS 75
OY 63 HKPYSGTVAVAFRSDITNOCYQELSEBERENCTHRSSVFGC--KVETTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYQTIEFSCPRIFNNAFSCCLKVKSHESQLRINS 132
OY 121 PPHPEKLTIRNRPNDSCGFYIVRLDDTKREPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKRNDSCGFYIVRQLENNK--TDVFGIPAFIYSF 175

RESULT 11
O91335 ID O91335 PRELIMINARY: PRT: 259 AA.
AC O91335:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Glycoprotein I.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DFD-6;
RA MEDLINE=98455388; PubMed=9784067;
RA Nishikawa Y., Xuan X., Otsuka H.;
RT "Identification and characterization of the glycoprotein E and I genes
RT of canine herpesvirus."
RL Virus Res. 56:77-92(1998).
DR EMBL: AB003728; BAA33764.1;
DR InterPro: IPR002874; Herpes_gI.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF01688; Herpes_gI.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 259 AA: 29965 MW; 66C7A9A957FF7E0F CRC64;

Query Match 7.9%; Score 147; DB 12; Length 259;
Best Local Similarity 27.3%; Pred. No. 3.3e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGVITGNHVSARIDDDHIVAPRPAATIQQLFFMPGQR-P-62
DB 16 LITMFLPTLFLFYGNGFYKGYISMFLNTSSGFSIFPDOKFVSGRLFLDDQHLS 75
OY 63 HKPYSGTVAVAFRSDITNOCYQELSEBERENCTHRSSVFGC--KVETTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYQTIEFSCPRIFNNAFSCCLKVKSHESQLRINS 132
OY 121 PPHPEKLTIRNRPNDSCGFYIVRLDDTKREPIDVFAIQLSVYOF 165

```

DB 133 IENGVLLEITNPKRNDGSGVFYRVOLENNK--TDVFGIPAFYSF 175

RESULT 12

ID 086789 PRELIMINARY: PRT: 370 AA.

AC 086789;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glycoprotein gI.

OS Feline herpesvirus (field herpesvirus 1).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

OX NCBI_TaxID=10334;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94267406; PubMed=8207390;

RA Spatz S.J., Kota P.A., Maes R.K.;

* Identification of the feline herpesvirus type 1 (FHV-1) genes encoding glycoproteins G, D, I and E: expression of FHV-1 glycoprotein D in vaccinia and raccoon poxviruses.*;

J. Gen. Virol. 75:1235-1244(1994).

DR EMBL: S72415; AAB30961.1; -

DR Interpro: IPR002874; Herpes_gI.1.

DR Pfam: PF01688; Herpes_gI.1.

SQ SEQUENCE 370 AA; 41568 MW; 2A816ECB37466A77 CRC64;

Query Match 7.8%; Score 145; DB 12; Length 370;

Best Local Similarity 22.0%; Pred. No. 8.1e-05;

Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

OY 5 LGTLALATLAFPGAMGIVITGNHVSARIDDDHIVAPRP-ATIQQLFPMPCQ-RP 62

DB 1 MSIAITYLIMATGYVYRGDHSVSLHNDTSSGFVITPLENFTLIGLILDDQPLP 60

OY 63 HKYSGTVKAFASDITNOCYOLSEERENCNHRSSSVFVGC--KYTEYFSA-SNRLTG 120

DB 61 VNNYNGTLEI-INYHNSCYKIVQVIEYSSCPRVNNAFRSCLHNTSMHQDLSINTS 119

OY 121 PRHPFLITRNPRNDGSGVFYRVDLDRKPIDVFAIQLSYQFANTATRLYSKASC 180

DB 120 VERGMLLTITSPKMDGGLIALVNRNNHNNK-ADVFGLSVYFSF----DFGRHHADE 174

OY 181 RTFG--LPTVQ--LEAYLRTEESWRNMQAY--VATEATTSABATTPPYATASASELA 234

DB 175 NLNGELITTPSPMETYVKV-----NTPYDHWYTTQTTSKMSSEPSNNTSISC----- 223

OY 235 EHRTFPMLENGVDHYEPTPANENSNTVRL-----GYSPTLIGVTVA 278

DB 224 -----HTFQNDPNEGETLYTHLNTAGNITYDDVMVMDGTTLKPRLI----- 264

OY 279 VVSATIGLVIVISITVRNNCTPHRKLD 306

DB 265 ----DMGLNLSTVSFFK--GNHAKMDT 286

RESULT 13

ID 091E39 PRELIMINARY: PRT: 369 AA.

AC 091E39;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Glycoprotein I.

GN US7

OS Phocid herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

OX NCBI_TaxID=47418;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PB84;

RA Martina B., Osterhaus A.D.M.E., Harder T.C.;

RT *Identification and analysis of immunogenicity of the glycoprotein D equivalent within the unique short segment of phocid herpesvirus-1.*;

RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ290955; CAC51466.1; -

DR Interpro: IPR002874; Herpes_gI.1.

DR Pfam: PF01688; Herpes_gI.1.

SQ SEQUENCE 369 AA; 42372 MW; 1587181704A7A8A CRC64;

Query Match 7.5%; Score 140.5; DB 12; Length 369;

Best Local Similarity 25.1%; Pred. No. 0.00021;

Matches 57; Conservative 36; Mismatches 89; Indels 45; Gaps 10;

OY 22 GIYITGNHVSARIDDDHIVAPRP-EATIQQLFPMPCQ-RPHKYSCTVAFASDIT 79

DB 16 GIYRGTYSMTMYNTSSGVIYVPPDDRFNTGVLLEDDQRLPVTNYSGITETIY---FN 72

OY 80 NCCYOLSEERENCNHRSSSVFVGC--KYTEYFSA---SNRLTGPPHPFLITRNPR 133

DB 73 YSCYTYVQTEYVSCPRHNNNAFRSCLIKVSKHQSLRINSIETG---VLEIKNPK 128

OY 134 PMSGAFYIVRLDDTKRPIDVFAIQLSYQFANTATRLYSKASCRTFGLPTVQLEAY 193

DB 129 PSDSGVYIFRVQLENNK--TDVFGISAFYVSFKSG--ENITRPDSNQT----- 173

OY 194 LRTEESWRNMQAYVATEATTSAA-----TTPPYATASASEL 232

DB 174 -----ENFTNHLVTPSTTISTKPSSESHLNTFTFDIPAPCHEV 213

RESULT 14

ID 039505 PRELIMINARY: PRT: 382 AA.

AC 039505;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glycoprotein I.

GN US7

OS Bovine herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

OX NCBI_TaxID=10320;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JURA;

RA Goltz M., Buhk H.J., Broll H., Lewin M., Mankertz A., Boerner B., Borchers K., Weigelt W.;

RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.

RN [12]

RP SEQUENCE OF 372-382 FROM N.A.

RC STRAIN=JURA;

RA Schwyzer M.;

RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.

RN [13]

RP SEQUENCE FROM N.A.

RC STRAIN=JURA;

RA Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J., Lowery D.E., Simard C., Bello L.J., Thiry E., Vlack C.;

RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.

RN [14]

RP SEQUENCE FROM N.A.

RC STRAIN=COOPER;

RA Goltz M., Buhk H.J., Schwyzer M.;

RT *Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome.*;

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ004801; CAA06146.1; -

DR EMBL: Z98199; CAB10890.1; -

DR Interpro: IPR002874; Herpes_gI.1.

DR Pfam: PF01688; Herpes_gI.1.

SQ SEQUENCE 382 AA; 39596 MW; 0F06C95CD2581EC2 CRC64;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:14:43 : Search time 16.5 Seconds
(without alignments)
1893.078 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863

Sequence: 1 MASLIGTALIAATLAPFGA.....VEIVAIYVPSALSSPSIKM 362

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328255 seqs, 8628685 residues

tal number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications: AA:*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*

2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*

8: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*

9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*

12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*

13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	10	US-09-881-457A-5
2	148	7.9	364	9	US-10-156-275-56
3	115	6.2	612	9	US-10-125-652-10
4	112	6.0	387	9	US-10-114-893-133
5	108	5.8	713	10	US-09-801-368-408
6	102.5	5.5	379	9	US-09-813-153-138
7	97	5.2	1220	10	US-09-801-368-332
8	93	5.0	320	9	US-09-738-626-5621
9	92.5	5.0	547	10	US-09-753-436-1
10	91	4.9	365	9	US-09-870-759-73
11	90.5	4.9	359	9	US-09-978-295A-45
12	90.5	4.9	359	9	US-09-978-697-45
13	90.5	4.9	359	9	US-09-978-192A-45
14	90.5	4.9	359	9	US-09-999-832A-45
15	90.5	4.9	359	9	US-09-978-189-45
16	90.5	4.9	359	9	US-10-174-590-42
17	90.5	4.9	359	9	US-10-176-758-42
18	90.5	4.9	359	9	US-10-175-737-42
19	90.5	4.9	359	9	US-10-173-706-42

20	90.5	4.9	359	9	US-10-175-738-42	Sequence 42, Appl
21	90.5	4.9	359	9	US-10-175-752-42	Sequence 42, Appl
22	90.5	4.9	359	9	US-10-176-482-42	Sequence 42, Appl
23	90.5	4.9	359	9	US-10-176-757-42	Sequence 42, Appl
24	90.5	4.9	359	9	US-10-176-913-42	Sequence 42, Appl
25	90.5	4.9	359	9	US-10-180-557-42	Sequence 42, Appl
26	90.5	4.9	359	9	US-10-180-557-42	Sequence 42, Appl
27	90.5	4.9	359	9	US-10-173-700-42	Sequence 42, Appl
28	90.5	4.9	359	9	US-10-174-576-42	Sequence 42, Appl
29	90.5	4.9	359	9	US-10-174-582-42	Sequence 42, Appl
30	90.5	4.9	359	9	US-10-174-588-42	Sequence 42, Appl
31	90.5	4.9	359	9	US-10-175-739-42	Sequence 42, Appl
32	90.5	4.9	359	9	US-10-175-740-42	Sequence 42, Appl
33	90.5	4.9	359	9	US-10-175-743-42	Sequence 42, Appl
34	90.5	4.9	359	9	US-10-176-488-42	Sequence 42, Appl
35	90.5	4.9	359	9	US-10-176-492-42	Sequence 42, Appl
36	90.5	4.9	359	9	US-10-176-747-42	Sequence 42, Appl
37	90.5	4.9	359	9	US-10-176-750-42	Sequence 42, Appl
38	90.5	4.9	359	9	US-10-176-885-42	Sequence 42, Appl
39	90.5	4.9	359	9	US-10-176-987-42	Sequence 42, Appl
40	90.5	4.9	359	9	US-10-176-991-42	Sequence 42, Appl
41	90.5	4.9	359	9	US-10-176-992-42	Sequence 42, Appl
42	90.5	4.9	359	9	US-10-176-993-42	Sequence 42, Appl
43	90.5	4.9	359	9	US-10-184-658-42	Sequence 42, Appl
44	90.5	4.9	359	9	US-10-173-695-42	Sequence 42, Appl
45	90.5	4.9	359	9	US-10-173-695-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-09-881-457A-5

Sequence 5, Application US/09881457A

Patent No. US20020081316A1

GENERAL INFORMATION: Mark D

APPLICANT: COCHRAN, Stephanie M

APPLICANT: WILD, Matthew A

TITLE OF INVENTION: NO. US20020081316A1el Avian Herpes Virus and Uses Thereof

FILE REFERENCE: ST0110510XOR

CURRENT APPLICATION NUMBER: US/09/881,457A

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 09/426,352

PRIOR FILING DATE: 1999-10-25

PRIOR APPLICATION NUMBER: 08/804,372

PRIOR FILING DATE: 1997-02-21

PRIOR APPLICATION NUMBER: PCT/US95/10245

PRIOR FILING DATE: 1995-08-09

PRIOR APPLICATION NUMBER: 08/663,566

PRIOR FILING DATE: 1996-06-13

PRIOR APPLICATION NUMBER: 08/288,065

PRIOR FILING DATE: 1994-08-09

PRIOR APPLICATION NUMBER: PCT/US93/05681

PRIOR FILING DATE: 1993-06-14

PRIOR APPLICATION NUMBER: 08/023,610

PRIOR FILING DATE: 1993-02-26

PRIOR APPLICATION NUMBER: 07/898,087

PRIOR FILING DATE: 1992-06-12

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 362

TYPE: PRT

ORGANISM: Infectious Laryngotracheitis Virus

US-09-881-457A-5

Query Match 100.0% Score 1863; DB 10; Length 362;

Best Local Similarity 100.0% Pred. No. 5.5e-166;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MASLIGTALIAATLAPFGAGYITGNHSAIDDDHIVYVAPPEATLOLOFPMPQ 60

Db 1 MASLGLTALLATLAPFGAMGIVITGNVARSARIDDDHVIYAPREATTIOLOLFMPGQ 60
Qy 61 RHHPKPGTVAFAFRSDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTSASNRLTG 120
Db 61 RHHPKPGTVAFAFRSDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTSASNRLTG 120
Qy 121 PHHPFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSVYQFANTATRGYSKASC 180
Db 121 PHHPFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSVYQFANTATRGYSKASC 180
Qy 181 RFGGLPTVLEAVLRTESRMNOAVATATTSATTPPVATTSASELEAHEFTFP 240
Db 181 RFGGLPTVLEAVLRTESRMNOAVATATTSATTPPVATTSASELEAHEFTFP 240
Qy 241 WLENGVDHEPTPANENSVTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCJP 300
Db 241 WLENGVDHEPTPANENSVTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCJP 300
Qy 301 HRKLDIVSODDERSGTRRESKRGPMVACEINKGADDOSELVELVAIYNPSALSSPDSI 360
Db 301 HRKLDIVSODDERSGTRRESKRGPMVACEINKGADDOSELVELVAIYNPSALSSPDSI 360
Qy 361 KM 362
Db 361 KM 362

RESULT 2
US-10-156-275-56
Sequence 56, Application US/10156275
Publication NO. US2003004944A1
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/156,275
FILING DATE: 28-May-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/399,118
FILING DATE: <unknown>
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-156-275-56

Query Match 7.9%; Score 148; DB 9; Length 364;
Best Local Similarity 27.3%; Pred. No. 1e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

Qy 4 LGTALLATLAPFGAMGIVITGNVARSARIDDDHVIYAPREATTIOLOLFMPGQ-P 62
Db 16 LITMFLPPLFLVGNDFVYKGYISMLNLSGFSIFPDOKFTVSGRLFLDDQHUS 75
Qy 63 HRPGTVAFAFRSDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTSASNRLTG 120
Db 76 VNNYSTIEFI--HNNCITYPTTYQTEYFSCRIENNMFRSLKVKVSHHESQULINS 132
Qy 121 PHHPFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSVYQF 165
Db 133 IENGVLLEITNRPNDSGVYFIRVQLENNK--TDVGIAPAFIYSF 175

RESULT 3
US-10-125-692-10
Sequence 10, Application US/10125692
Publication NO. US2003004429A1
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
APPLICANT: Ozlinsky, Adrian
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
FILE REFERENCE: P-IS 5155
CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 612
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-692-10

Query Match 6.2%; Score 115; DB 9; Length 612;
Best Local Similarity 20.6%; Pred. No. 0.026;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

Qy 19 GAMGIYITNHSARIDDDHVIYAPREATTIOLOLF--FMPGQPHKPGTVAFAFR 75
Db 93 GSPFLIT--NKLKMEISQYICELNKE--EVELWYFKYTFSGTSLLOGSITLILDSN 149
Qy 76 SDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTSASNRLTGPHPFKLTIRNRPN 135
Db 150 SKVSN---PLTE---CKHKKGVSGSKV-----LSMSNLRVQ 181
Qy 136 DSGMFYIVRLDDTKPEIDVFAIOLSVYQFANTATRGYSKASCTPGLPVLQLEAVLR 195
Db 182 DDDFMNCTVTLDDKK--NMFGMTLSVLGFOSYALT-AVKSSESSEFSPLNFAE---- 233
Qy 196 TEESWRN--WQAVVATEATTSAEATTPPVATTSASELEAHEFTFPLENGVDHEPTP 253
Db 234 -ENGCELMMKA-----EKSFQPMVFSISKKEVSV 265
Qy 254 ANENSVTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCJPARKLDIVSODDEE 313
Db 266 OKSTDKLQLKELPLTLTKIPVSHQFAGSGL---TLTLDKGLHQEVNLYVKKVQ 321
Qy 314 RSQTRRESKRGPMVACEIN-----KGADOD---SELVELVAIYNPSA----- 353
Db 322 LNNI-----LTCEVMGPTSPKRMRLTLQENDEARVSEOKVQVYVABETGLMOCL 371
Qy 354 LSSPDSIKM 362
Db 372 LSEGDVKM 380


```
RESULT 4
US-10-114-893-133
; Sequence 133, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalley, Edward R.
; APPLICANT: Collins-Reche, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merdey, David
; APPLICANT: Bowman, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, Mckeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-133

Query Match
Best Local Similarity 19.2%; Pred. No. 0.026;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

        6.0%; Score 112; DB 9; Length 387;
OY 1 MASLIGTALAAATAPGAMGIVITGNHVSARIDDDHIVARPRATTQDLFPMQO 60
DB 12 LSCLAGVSVQVYI-PDGFVNVVGSNTLLCI---YTTVASRQSLSIOWSF----- 62
OY 61 RPKRPYSGTVARAFSDITNOCYELSEEFENCRRSSSVFVGCXKTEFTFSASRLTG 120
DB 63 --HKMEPISIVF-----SGGQNAVAIG-----QFKDRITG 92
OY 121 PPHP--FKLTINPRPNDSGMFYIYVLDTKEPIDVRIQLSLYQFANRANRAGLYSKRA 178
DB 93 SNDGNASTISHMQPADSGIY---TCVNNPDPFLGONGILNNSVLKRP-----SKP 143
OY 179 SCRTFGIP---TVOLEAVLTESMRNMOAYVATATTSSEATTPPTATISASELEA 234
DB 144 LCSVGRPETGHTISLCL-----SALGTFSPVY-----RLG----- 171
OY 235 EHFTFPWLENGVDHYEPTPANNSNVTV-----RLG----- 265
DB 172 ---YVW--HKLEGRDIYVENENPTTGLIVTGNLTNEGGYVOCYCTAINLGSCEID 225
OY 266 -TMSPTLIGVTAVAVSAVATIGIVISIVTRNNCTPHRKLDTVSODDEERSQTRRESKRF 324
DB 226 LTSHPREVGIYVAGALIGSLVCAIIISIV---CFARNKAKAKAK--ERNKTIYAE---L 276
OY 325 GPMVACEINKGADODS---ELVEIYVAIVNPSAL--SSPDSIK 361
DB 277 EPWT--KINRGESEAMPREDATQLEVTLPSSIHETGPPITQ 316

RESULT 5
US-09-801-368-408
; Sequence 408, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busdy, Robert
; APPLICANT: Call, Brian
```

```
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 408
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-408

Query Match
Best Local Similarity 27.3%; Pred. No. 0.15;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

        5.8%; Score 108; DB 10; Length 713;
OY 60 QRPKRPYSGTVARAFSDITNOCYELSEEFENCRRSSSVFVGCXKTEFTFSASRLTG 115
DB 86 QRPKRPYSGTVARAFSDITNOCYELSEEFENCRRSSSVFVGCXKTEFTFSASRLTG 144
OY 116 NRTGSPHPEKLTINPRPNDSGMFYIYVLDTKEPIDVRIQLSLYQFANRANRAGLYSKRA 197
DB 145 NRTGSPHPEKLTINPRPNDSGMFYIYVLDTKEPIDVRIQLSLYQFANRANRAGLYSKRA 208
OY 155 VFAIQLSVQVANTANRAGLYSKRASCRTGELPTVOL-BAIYLTESMRNMOAYV-----A 208
DB 198 QRPKRPYSGTVARAFSDITNOCYELSEEFENCRRSSSVFVGCXKTEFTFSASRLTG 254
OY 209 TEATTTSAEAT--TPTPVATSAEAEHFTFPWLENGVDHYEPTP 253
DB 255 TEATTTSAEAT--TPTPVATSAEAEHFTFPWLENGVDHYEPTP 299

RESULT 6
US-09-813-153-138
; Sequence 138, Application US/09813153
; Publication No. US20030045459A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023
; CURRENT APPLICATION NUMBER: US/09/813,153
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US/09/363,044
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,161
```

PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,170
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 138
LENGTH: 379
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (379)
OTHER INFORMATION: Xaa equals scop translation
US-09-813-153-138

Query Match
Best Local Similarity 23.6%; Pred. No. 0.2; Length 379;
Matches 73; Conservative 36; Mismatches 133; Indels 67; Gaps 13;

65 PVSIGVAVAFRSDITNOCYQELSEERFENCNTHRSSVFGCKVTEYTFSSANRLTG--PP 122
|||
60 PYSCKEALIRTD-----CMRVTSRK-SAKYRLQGTIPR 92
|||
QY 123 HPRKLTIRPNRPNDSGMFYIVRL---DDTKRPIDVFAQLSVQFANTAAIRGLYSKA 178
|||
DB 93 GDVSLTILNPSSEDSGVCCRIEVPGFMDVK-----INRLNL-ORASTTHTATATTT 146
|||
QY 179 SCRTFGLPTVQLEAVLRTEESMRNMOAVYATEATTSAEATPTP-----VTATSASE 231
|||
DB 147 RRTTTSPT-----TTRQMTTPALPTTYVT-PDITTCPTLOMTIANFTTANNC 197
|||
QY 232 LENAHTFPMLENGVHYEPTPANENSNTVRLGTMSPILIGTVAAVVSATIGLVIVIS 291
|||
DB 198 LSLTPSTLP-EBATGLTPPEPSKGPILTAESEIVLPSSMSAESTSADTFLTSKES 255
|||
QY 292 IYTRNCTPH---RKLDPVSDODEERSOT---RRESRKFQGMVACEINKGADDOSEIV 343
|||
DB 256 KWDLPSTSHVSMKTSDSVSPQASDTAVPEQNKTKTGQMDG--IPMSKNEPIS 313
|||
QY 344 ELVAIVNPS 352
|||
DB 314 QLLMITAPS 322
|||

RESULT 7
US-09-801-368-332
Sequence 332, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 332

LENGTH: 1220
TYPE: PRF
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match
Best Local Similarity 22.7%; Pred. No. 3.3; Length 1220;
Matches 58; Conservative 43; Mismatches 104; Indels 50; Gaps 11;

5 LGTLLAATLAPGAMGYITGNHVSARIDDIYIVAPRPATIQLOLFMPGGRPHK 64
|||
DB 32 LGSLLILAVT-----TGVIYSNKNLR--SDRLYIAQLKSSQIDQTLNLT-----YIO 79
|||
QY 65 PVSIGVAVAFRSDITNOCYQELSEERFENCNTH---RSSVFGCKVTEYTF--SA 114
|||
DB 80 AYLARDAQLQSLTGYVAGNKSADNMVDSLVYQKFLSSNLFYAKYDSSFNVLNA 139
|||
QY 115 SNRLTGPPHP-----FKLTIRPNRPNDSGMFYIVRLDDTKRPIDVFAQLSVQFAN 167
|||
DB 140 TNNGTDLIPEDVLDLPLSTDTPLP--SLLETIGILDVPLNSTD-YLMSLSLPIFAN 196
|||
QY 168 TAATRGLYSKASCRTPGLPTVQLEAVLRTEESMRNMOAVYATEATTSAEATPTPTAT 227
|||
DB 197 PSII-----LTDSRYVGYITIIIMSA-----EGLSVFNDDTALHSHIATISAV 240
|||
QY 228 SASELEAE--HETFP 240
|||
DB 241 YNSQKASGYHVEFP 255
|||

RESULT 8
US-09-738-626-5621
Sequence 5621, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5621
LENGTH: 320
TYPE: PRF
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5621

Query Match
Best Local Similarity 20.6%; Pred. No. 1.2; Length 320;
Matches 62; Conservative 46; Mismatches 109; Indels 84; Gaps 14;

100 SYFVGCKVTEY-----TFSSANRLTGPPH-----PKLTIRPNRPNDSGMFYIVRL 146
|||
DB 56 AVFPAPEISHYMLVTF-----GLPHEIIPVAGPIPMHLMRDAGNET-----KF 102
|||
QY 147 DDTKRPIDVFAQL---SVYQFANTAAIRGLYSKASCRTPGLPTVQLEA-YLRTEESMRN 202
|||

Tue May 6 18:37:37 2003

us-09-993-777-7.rapb

Page 5

Db 103 KDSMPDLVSOALILRLDLYVRRAEDAMVLLGG-----NLPSIAPAMFVDVVRSLRL 155
QY 203 MOAVVATEATTSA-----EATPTPTVATTS-----ASELPAHEFTFPMLGVH 248
Db 156 YHPVKAIAATGALRAVIRQLATSPDLIVAAEEIIRATGLEPKLRGPVVE-----210
QY 249 KEPTPANENSVTVRLGTWSPPLIGVVAVVSATIGLVISIVTRNMCTPHRKLDYVS 308
Db 211 -----GDLSPV--AAARALIDSGVTEVLTKRKRESLYVSESESLAS 252
QY 309 ODDEBSQ--TRESKRKRPYACINKGADODELVEIVAVNPSA-----LSPDSI 360
Db 253 YDSTPGKQGVNREFTAGFLAAS--NDGKTEDSVINAVAAVAMGSEMDNYIPTPDKL 310
QY 361 K 361
Db 311 R 311

SEQUENCE 9
-09-753-436-1
Sequence 1, Application US/09753436
Patent No. US2001002923A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemary
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09753, 436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382, 289
FILING DATE:
APPLICATION NUMBER: US 08/487, 113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286, 754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102, 852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009, 266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894, 061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889, 724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827, 689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 30..547
US-09-753-436-1

Query Match
Best Local Similarity 23.3%, Pred. No. 2.8;
Matches 69; Conservative 36; Mismatches 80; Indels 111; Gaps 15;

QY 103 VGCKVTEYTFASNRRLTGPHPFKL-----TIR-----NRPNDGMYIY 143
Db 98 VYCNQSGOITGSSNITVYGLPERVELAPLPMPQVGNFTLRQVBSGR--TSLTVL 154
QY 144 VLDD-----TKEPIDVFAIQLS-----VYOFANTAATRGLY 175
Db 155 LWEEELSRQPAVEPEAVTATVLSRDDHGAFCSCRTLEDMQPGILFVNTSAPQL- 213
QY 176 SKASCRTEGLPTV--OLEA--YLTEESW-----RNMQAVVA-----TEATTT 214
Db 214 -----RTPLVLPVPPRLVAPRFLEVETSWPDCITLDGLFPASBAQYIALGDOMINATVM 268
QY 215 SAETTPPTPVNTSASELA-----EHT-FPMLGVHDYEPPTPAN 255
Db 269 NNGDILATATATARAQDEGAREIVCNVTLGERREARENUTVFSPLGIVALSPT-AH 327
QY 256 ENSNTVRLGTRSPPLIGVVAVVSATIGLVISIVTRNMCTPHRKLDYSDO 311
Db 328 EGSTVTV--SCMAGARVQVTLIDGVPAARQ-----TAQLQINATRESDD 369

RESULT 10
US-09-870-759-73
Sequence 73, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870, 759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208, 128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 73
LENGTH: 365
TYPE: PRT
ORGANISM: Mus musculus
US-09-870-759-73

Query Match
Best Local Similarity 20.4%, Pred. No. 2.2;
Matches 78; Conservative 52; Mismatches 128; Indels 124; Gaps 19;

QY 50 IOLDLPMFGORPHK-----YSGTVV-----AFRSDINOCY 83
Db 15 LQSL-----AHPHOIDLNTCTRYAGVFEVKNRGYSISRTREADLCOAFNSTLPTMQ 69
QY 84 OELS-ERRPNC-----THRSSVVGCKVTE--YTFASNR 117
Db 70 MKLAKSGFETCYGFEIGNVYIRIHPNACANHTGVILVNTSHTDYCFNAS-- 127
QY 118 LTGPPEPKLTIRN-PRPDSGMPFVYVRLDDK-----EPIDVAIOLSVYGF 165
Db 128 --APPEDCTSVTLDPNSFDGCVITITVYNNRGTRYSKKEGYRTHQEDIDASNI-----I 179

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085697
Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2, 4; 113; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches 117; Gaps 16;
5 LGTL-----ALLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIQLQIF-----55
16 LGVLVAAQMLLAASFETLQCEPVCCT--EESCHTEDD---LTDNAEAGFVKAYTESEP 70
56 -----FMGQRPKP--YSGVNAVAPRSDITNOCYOELSEBERFNCNTHSSSVFVCK 106
71 FLHLYSYMWLLQSPAKPVEBDDLVL-----LRQAMQD-----WP 106
107 VRETFYSNRLNGPBP---FKLTIRNDRNDGMY-----YIVR 145
107 LVQVTFYFDGSGALPFPNREFSITV--VQADSGHHCSGIFQSPGPIPETASVAIT 164
146 LDD-----TKEPIDVFAIOL--SYQFANTATRGATYSK 177
165 VOELFPADILRAVPSAEPOAGSPMILSCOTKLPLORSNAHLTFYKDKGRIVQSGLSSE 224
178 ASCTRTGFLPTVQ-----LEAYLTRESNR--NMQAYVATEATTSAATTPPTVATS 228
225 -----FOIPFASSEDHSGSYWCENATEDNOMKQSPOLEIRVQAGASSA-----APTLNP 274
229 ASELAEHETFPWLENGVDHYEPTPANENSNTVRLGTMSFTL 271
275 APQKSAAPGTAEAPAPGLPPLPPTPSSSDPGFSSLPMPDPL 317
RESULT 12
US-09-978-697-45
Sequence 45, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Fritman, Napoleon
APPLICANT: Flitcroft, Ellen
APPLICANT: Fony, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249


```

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 21.0%; Score 90.5; DB 9; Length 359;
Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

5 LGTL-----ALLAATLAFGAMGIVITGNHVSARIDDDHIVAVAPRATLOLE----- 55
16 LGVLVAGMLAASFELQCEGPVCT-ESSCHTEDD-----LTDAREAGQVAYTFSEP 70
QY 56 -----FMGQRPKRP-YSCTVRAFRSDITNOCYELSEEFENCETRSSSVYVCK 106
DB 71 FHLYISYDMLIOGPAKPVTEGLV-----LRCQAMOD-----WP 106
QY 107 VHEYFASNRLTGPHP---FKLITRNPDPDSGMY-----VYVR 145
DB 107 LTQVTFYDGSALGPDPNREFSIV--VQKADSGHYHCSGIFSGPGGIPETASVVAIT 164
QY 146 LDD-----TKEPIDVFAIOL--SVYQAFNTAATNGLYSK 177
DB 165 VOELFPADILRAVPSAPQASPMILSCQTKLPLORSAAKLFFEFYDGRIVOSRLSE 224
QY 178 ASCRTFGLPTVO-----LEAYLTRESNR-NMQAVVATEATTTSAAETPTPTATIS 228
DB 225 -----FOIPTASEDHSSGYCEATDNQVMQSPQLEIRVOGASSSA-----APETLNP 274
QY 229 ASELAEHFTFPMLENGVDHYEPTPANENSNTVRLGTMSPTL 271
DB 275 AFQKSAAPGTAPBEAPCPPLPPPTPSSEDPGFSPLGMPDHL 317

RESULT 13
US-09-978-192A-45
; Sequence 45, Application US/09978192A
; Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
```

PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4; Mismatches 113; Indels 117; Gaps 16;
Matches 72; Conservative 41;

OY 5 LGTL---ALATLAPFGAMGIVITGNHVSARIDDDHIVAPREARTIQLQF-----55
DB 16 LGVLWVAQMLASFEFLQCEGPVCT-EESCHTEDD---LTDAREAGVQAVATFSEP 70
OY 56 -----FMPGQRPKRP-YSGTVRVAFRSDITNOCYQELSEERFENCRTHRSSVVGCK 106
DB 71 FHLIVSYDWLILQGPAPKPFEGDLV-----LRCQAMOD-----WP 106
OY 107 VREYTFASNRNLGPPHP---FKLITRNPRPNDGMEY-----VIYR 145
DB 107 LIOVTFYRQGSALGPPGPNREFSITY--VOKADSGHYHCSGIRPSGPGIPEASVVAIT 164
OY 146 LBD-----TRKPIDVFAIQL--SVYOFANTAAATRLGLSK 177
DB 165 VOELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAAARLFSFYKDGRIYOSRGLSSE 224
OY 178 ASGRTFGLPYQ-----LEAYLRTESMR-NMQAYVATEATTSAEATPTPTATNS 228
DB 225 -----FOIPTASEDHSGSTWCENATEDNOVMKOSPQLEIRVQAGASSA-----APPTLNP 274
OY 229 ASLEAEHFTFPWLENGVDHYEPTPANENSNTVRLGTMSPTL 271
DB 275 APQKSAAPGTAPAEAPGPIPPPTPSSDDPGFSSPLGMPDPHL 317

RESULT 14
US-09-999-832A-45
Sequence 45, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT FILING DATE: 2001-10-24
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match Best Local Similarity 4.9%; Score 90.5; DB 9; Length 359;
Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

QY 5 LGTL---ALLAATLAPFCAMGIVITGNHVSARIDDDHIVAPREATTOLQF-----55
DB 16 LGVLWAOQLLAASFETLQCEGPVCT-ESSCHTEDD---LTDAREAGFOVAVYFSESP 70
DB 56 -----FMPOQRPKP-YSGTVARAFRSDITNOCYQELSEERFENCNHRSSVYVGCK 106
DB 71 FHLIVSYDWLILQGPAPKPVFEGLDV-----LRQAMOD-----WP 106
QY 107 VTEYFESASNRLLTGPHP---FKLTIRNRPNDGMY-----VIVR 145
DB 107 LTVGYFTRGSLGALPGPRNREFSITY--VQKADSGHYHCSGIFQSPGPIPETASVVAIT 164
QY 146 LDD-----TKEPIDVFAIQL---SVYQAFNATATRLYSK 177
DB 165 VOELFAPAPILRAVPSAEPOAGSPMTLSCQTKLPLQRSARLLFSEYKDGRIYQSRLSSE 224
QY 178 ASGRFTGLFTVQ-----LEAYLRTESWR-NMQAYVATEHTTTSAETPTPTATSS 228
DB 225 -----FOITASEDSHSGSYWCEATEDNOMKOSPOLETRVQGAASSA-----APPTLMP 274
QY 229 ASELEAEHFTPMLENGVDHYEPTPANENSNTVRLGTWSPTL 271
DB 275 APOKSAAPGTABEAPGPIPRPTFSSSEDPGESSPLGMPDPL 317

RESULT 15
US-09-978-189-45
; Sequence 45, Application US/09978189

;; Publication No. US20030004102A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertlisen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kilavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James J.
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumaw, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC7
;; CURRENT APPLICATION NUMBER: US/09/978.189
;; PRIOR FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078004
;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match

4.9%; Score 90.5; DB 9; Length 359;

Best Local Similarity 21.0%; Pred. No. 2.4; Indels 117; Gaps 16;

Matches 72; Conservative 41; Mismatches 113;

QY 5 LGTT---ALMATLAPFGANGIVITGNHVSARIDDDHIVIAAPPETIOLQF-----55
DB 16 LGVIAWQMLAASFETIQCCEPVCT-EESSCHTEDD---LTDAREAGFOVKAYTSEP 70
QY 56 -----EMPGORPKP-YSGTVAVAFRSQITNOCYOEISBERENCTHSSSVFVGCK 106
DB 71 FHLIVSTDWLLILOGPAKVFEBDDLY-----LKCQAMOD-----WP 106
QY 107 VTEYTESASNRKLTGPHP---FKLIRNPRNNSGMFY-----VYR 145
DB 107 LTQVTFYRDSALGPPGPKREFSTIV-VQABSGHYHCSGLFQSPGCGIETASVVAIT 164
QY 146 LDD-----TKEPIDVFAIOL--SYQORANTMAIRGLXK 177
DB 165 VOELFPAPILRAVPSAEPOAGSPMTLSCQTKLPLQNSAARLFFSKQGRIVQNSGLSE 224

Tue May 6 18:37:37 2003

us-09-993-777-7.rapb

Page 14

[illegible]

Search completed: May 5, 2003, 16:26:30
Job time : 20.5 secs